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Fea

1: NM\_005191. Homo sapiens CD80...[gi:31377790]

Links

LOCUS NM\_005191 2824 bp mRNA linear PRI 22-DEC-2003  
DEFINITION Homo sapiens CD80 antigen (CD28 antigen ligand 1, B7-1 antigen)  
(CD80), mRNA.

ACCESSION NM\_005191  
VERSION NM\_005191.2 GI:31377790  
KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2824)

AUTHORS Clayton,A.R., Prue,R.L., Harper,L., Drayson,M.T. and Savage,C.O.  
TITLE Dendritic cell uptake of human apoptotic and necrotic neutrophils  
inhibits CD40, CD80, and CD86 expression and reduces allogeneic T  
cell responses: relevance to systemic vasculitis

JOURNAL Arthritis Rheum. 48 (8), 2362-2374 (2003)

PUBMED [12905492](#)

REMARK GeneRIF: Immature dendritic cells engulfed apoptotic and necrotic  
neutrophils, resulting in up-regulation of CD83 and class II major  
histocompatibility complex molecules, but down-regulation of CD40,  
CD80, and CD86

REFERENCE 2 (bases 1 to 2824)

AUTHORS Niu,H., Cattoretti,G. and Dalla-Favera,R.

TITLE BCL6 controls the expression of the B7-1/CD80 costimulatory  
receptor in germinal center B cells

JOURNAL J. Exp. Med. 198 (2), 211-221 (2003)

PUBMED [12860928](#)

REMARK GeneRIF: results show that BCL6 prevents CD40-induced expression of  
CD80 by binding its promoter region in vivo and suppressing its  
transcriptional activation by NF-kappaB

REFERENCE 3 (bases 1 to 2824)

AUTHORS Morichika,T., Takahashi,H.K., Iwagaki,H., Yagi,T., Saito,S.,  
Kubo,S., Yoshino,T., Akagi,T., Mori,S., Nishibori,M. and Tanaka,N.

TITLE Effect of prostaglandin E2 on intercellular adhesion molecule-1 and  
B7 expression in mixed lymphocyte reaction

JOURNAL Transplantation 75 (12), 2100-2105 (2003)

PUBMED [12829919](#)

REMARK GeneRIF: effect of PGE2 on the expression of ICAM-1 and B7 in the  
human mixed leukocyte reaction (MLR) in the presence or absence of  
IL-18

REFERENCE 4 (bases 1 to 2824)

AUTHORS Rogers,N.J., Jackson,I.M., Jordan,W.J., Hawadle,M.A., Dorling,A.  
and Lechler,R.I.

TITLE Cross-species costimulation: relative contributions of CD80, CD86,  
and CD40

JOURNAL Transplantation 75 (12), 2068-2076 (2003)

PUBMED [12829914](#)

REMARK GeneRIF: expression profiles and relative contribution in the  
porcine-human xenogeneic response

- REFERENCE 5 (bases 1 to 2824)  
AUTHORS Chen,X.L., Cao,X.D., Kang,A.J., Wang,K.M., Su,B.S. and Wang,Y.L.  
TITLE In situ expression and significance of B7 costimulatory molecules within tissues of human gastric carcinoma  
JOURNAL World J. Gastroenterol. 9 (6), 1370-1373 (2003)  
PUBMED [12800259](#)  
REMARK GeneRIF: ICOS-B7H costimulatory pathway may be involved in the negative regulation of cell-mediated immune responses.
- REFERENCE 6 (bases 1 to 2824)  
AUTHORS Grosenbach,D.W., Schlom,J., Gritz,L., Gomez Yafal,A. and Hodge,J.W.  
TITLE A recombinant vector expressing transgenes for four T-cell costimulatory molecules (OX40L, B7-1, ICAM-1, LFA-3) induces sustained CD4+ and CD8+ T-cell activation, protection from apoptosis, and enhanced cytokine production  
JOURNAL Cell. Immunol. 222 (1), 45-57 (2003)  
PUBMED [12798307](#)  
REMARK GeneRIF: combined use of a vector driving the expression of OX40L with three other costimulatory molecules (B7-1, ICAM-1, and LFA-3) both enhances initial activation and then further potentiates sustained activation of nai;ve and effector T cells.
- REFERENCE 7 (bases 1 to 2824)  
AUTHORS Bernsen,M.R., Hakansson,L., Gustafsson,B., Krysanter,L., Rettrup,B., Ruiter,D. and Hakansson,A.  
TITLE On the biological relevance of MHC class II and B7 expression by tumour cells in melanoma metastases  
JOURNAL Br. J. Cancer 88 (3), 424-431 (2003)  
PUBMED [12569387](#)  
REMARK GeneRIF: On the biological relevance of MHC class II and B7 expression by tumour cells in melanoma metastases.
- REFERENCE 8 (bases 1 to 2824)  
AUTHORS Tatari-Calderone,Z., Semnani,R.T., Nutman,T.B., Schlom,J. and Sabzevari,H.  
TITLE Acquisition of CD80 by human T cells at early stages of activation: functional involvement of CD80 acquisition in T cell to T cell interaction  
JOURNAL J. Immunol. 169 (11), 6162-6169 (2002)  
PUBMED [12444120](#)  
REMARK GeneRIF: data suggest that CD80 acquisition by human T cells might play a role in the immunoregulation of T cell responses
- REFERENCE 9 (bases 1 to 2824)  
AUTHORS Ke,X.Y., Gribben,J., Wang,J. and Wang,D.B.  
TITLE The identical effects of B7-1 and B7-2 on regulation of human IL-2 gene transcription factors NF-kappa B and AP-1  
JOURNAL Zhongguo Shi Yan Xue Ye Xue Za Zhi 10 (6), 512-518 (2002)  
PUBMED [12513711](#)  
REMARK GeneRIF: The identical effects of B7-1 and B7-2 on regulation of human IL-2 gene transcription factors NF-kappa B and AP-1.
- REFERENCE 10 (bases 1 to 2824)  
AUTHORS Manzotti,C.N., Tipping,H., Perry,L.C., Mead,K.I., Blair,P.J., Zheng,Y. and Sansom,D.M.  
TITLE Inhibition of human T cell proliferation by CTLA-4 utilizes CD80 and requires CD25+ regulatory T cells  
JOURNAL Eur. J. Immunol. 32 (10), 2888-2896 (2002)  
PUBMED [12355442](#)  
REMARK GeneRIF: CD80 and CD86 differ in their interactions with CTLA-4 and that CD80 appears to be the preferential inhibitory ligand for CTLA-4 working via a population of CD4(+) CD25(+) CTLA-4(+) regulatory T cells.
- REFERENCE 11 (bases 1 to 2824)  
AUTHORS Akiyama,Y., Shirasugi,N., Uchida,N., Matsumoto,K., Kitajima,M.,

Bashuda,H., Yagita,H., Okumura,K., Aramaki,O. and Niimi,M.  
TITLE B7/CTLA4 pathway is essential for generating regulatory cells after intratracheal delivery of alloantigen in mice  
JOURNAL Transplantation 74 (5), 732-738 (2002)  
PUBMED 12352894  
REMARK GeneRIF: with ctla4 pathway, is essential for generating regulatory cells after intratracheal delivery of alloantigen in mice  
REFERENCE 12 (bases 1 to 2824)  
AUTHORS Wang,S., Veldman,G.M., Stahl,M., Xing,Y., Tobin,J.F. and Erbe,D.V.  
TITLE Antibodies to B7.1 define the GFCC'C' face of the N-terminal domain as critical for co-stimulatory interactions  
JOURNAL Immunol. Lett. 83 (2), 77-83 (2002)  
PUBMED 12067755  
REFERENCE 13 (bases 1 to 2824)  
AUTHORS Terrazzano,G., Zanzi,D., Palomba,C., Carbone,E., Grimaldi,S., Pisanti,S., Fontana,S., Zappacosta,S. and Ruggiero,G.  
TITLE Differential involvement of CD40, CD80, and major histocompatibility complex class I molecules in cytotoxicity induction and interferon-gamma production by human natural killer effectors  
JOURNAL J. Leukoc. Biol. 72 (2), 305-311 (2002)  
PUBMED 12149421  
REMARK GeneRIF: CD40 and CD80 molecules were observed to play a specific role in the induction of cytotoxic function but not in IFN-gamma production of IL-2-activated NK effectors.  
REFERENCE 14 (bases 1 to 2824)  
AUTHORS Venuprasad,K., Banerjee,P.P., Chattopadhyay,S., Sharma,S., Pal,S., Parab,P.B., Mitra,D. and Saha,B.  
TITLE Human neutrophil-expressed CD28 interacts with macrophage B7 to induce phosphatidylinositol 3-kinase-dependent IFN-gamma secretion and restriction of Leishmania growth  
JOURNAL J. Immunol. 169 (2), 920-928 (2002)  
PUBMED 12097397  
REMARK GeneRIF: Leishmania major infection of macrophages cocultured with neutrophils results in a neutrophil-macrophage interaction via CD80 leading to IFN-gamma secretion and restriction of Leishmania growth.  
REFERENCE 15 (bases 1 to 2824)  
AUTHORS Sellebjerg,F., Jensen,J., Jensen,C.V. and Wiik,A.  
TITLE Expansion of CD5 - B cells in multiple sclerosis correlates with CD80 (B7-1) expression  
JOURNAL Scand. J. Immunol. 56 (1), 101-107 (2002)  
PUBMED 12100477  
REMARK GeneRIF: expansion of CD5- B cells in multiple sclerosis correlates with CD80 (B7-1) expression  
REFERENCE 16 (bases 1 to 2824)  
AUTHORS Suvas,S., Singh,V., Sahdev,S., Vohra,H. and Agrewala,J.N.  
TITLE Distinct role of CD80 and CD86 in the regulation of the activation of B cell and B cell lymphoma  
JOURNAL J. Biol. Chem. 277 (10), 7766-7775 (2002)  
PUBMED 11726649  
REMARK GeneRIF: Thus, this study is the first demonstration of a distinct signaling event induced by CD80 and CD86 molecules in B cell lymphoma.  
REFERENCE 17 (bases 1 to 2824)  
AUTHORS Erbe,D.V., Wang,S., Xing,Y. and Tobin,J.F.  
TITLE Small molecule ligands define a binding site on the immune regulatory protein B7.1  
JOURNAL J. Biol. Chem. 277 (9), 7363-7368 (2002)  
PUBMED 11741888



REMARK      GeneRIF: specific small molecule inhibitors of human B7.1 were identified and characterized. These compounds inhibit the binding of B7.1 to both CD28 and CTLA4.

REFERENCE   18 (bases 1 to 2824)

AUTHORS     Vasilevko,V., Ghochikyan,A., Holterman,M.J. and Agadjanyan,M.G.

TITLE        CD80 (B7-1) and CD86 (B7-2) are functionally equivalent in the initiation and maintenance of CD4+ T-cell proliferation after activation with suboptimal doses of PHA

JOURNAL     DNA Cell Biol. 21 (3), 137-149 (2002)

PUBMED      [12015893](#)

REMARK      GeneRIF: CD80 and CD86 molecules can substitute for each other in the initial activation of resting CD4(+) T cells and in the maintenance of their proliferative response

REFERENCE   19 (bases 1 to 2824)

AUTHORS     Pesce,G., Fiorino,N., Riccio,A.M., Montagna,P., Torre,G., Salmaso,C., Altrinetti,V. and Bagnasco,M.

TITLE        Different intrathyroid expression of intercellular adhesion molecule-1 (ICAM-1) in Hashimoto's thyroiditis and Graves' disease: analysis at mRNA level and association with B7.1 costimulatory molecule

JOURNAL     J. Endocrinol. Invest. 25 (3), 289-295 (2002)

PUBMED      [11936473](#)

REMARK      GeneRIF: colocalization of ICAM-1 and B7.1 molecules was demonstrated in Hashimoto's thyroiditis whereas no B7.1 expression was observed in Graves' disease

REFERENCE   20 (bases 1 to 2824)

AUTHORS     Tzachanis,D., Berezovskaya,A., Nadler,L.M. and Boussiotis,V.A.

TITLE        Blockade of B7/CD28 in mixed lymphocyte reaction cultures results in the generation of alternatively activated macrophages, which suppress T-cell responses

JOURNAL     Blood 99 (4), 1465-1473 (2002)

PUBMED      [11830501](#)

REMARK      GeneRIF: Blockade of B7/CD28 costimulation in mixed lymphocyte reaction cultures results in the generation of alternatively activated macrophages, which suppress T-cell responses, and perhaps play a critical role in the induction of transplantation tolerance.

REFERENCE   21 (bases 1 to 2824)

AUTHORS     Niemann-Masanek,U., Mueller,A., Yard,B.A., Waldherr,R. and van der Woude,F.J.

TITLE        B7-1 (CD80) and B7-2 (CD 86) expression in human tubular epithelial cells in vivo and in vitro

JOURNAL     Nephron 92 (3), 542-556 (2002)

PUBMED      [12372936](#)

REMARK      GeneRIF: After B7-1 and B7-2 induction, proximal tubular epithelial cells costimulate CD28 on T lymphocytes resulting in cytokine production.

REFERENCE   22 (bases 1 to 2824)

AUTHORS     Chang,T.T., Kuchroo,V.K. and Sharpe,A.H.

TITLE        Role of the B7-CD28/CTLA-4 pathway in autoimmune disease

JOURNAL     Curr. Dir. Autoimmun. 5, 113-130 (2002)

PUBMED      [11826754](#)

REMARK      GeneRIF: The B7-CD28/CTLA-4 costimulatory pathway has a dominant role in regulating T-cell activation. Antagonists enable graft survival and suppress autoimmunity.

REFERENCE   23 (bases 1 to 2824)

AUTHORS     Reeves,R.H., Patch,D., Sharpe,A.H., Borriello,F., Freeman,G.J., Edelhoff,S. and Disteché,C.

TITLE        The costimulatory genes Cd80 and Cd86 are linked on mouse chromosome 16 and human chromosome 3

JOURNAL     Mamm. Genome 8 (8), 581-582 (1997)

PUBMED [9250865](#)  
REFERENCE 24 (bases 1 to 2824)  
AUTHORS Freeman,G.J., Disteché,C.M., Gribben,J.G., Adler,D.A.,  
Freedman,A.S., Dougery,J. and Nadler,L.M.  
TITLE The gene for B7, a costimulatory signal for T-cell activation, maps  
to chromosomal region 3q13.3-3q21  
JOURNAL Blood 79 (2), 489-494 (1992)  
PUBMED [1370389](#)  
REFERENCE 25 (bases 1 to 2824)  
AUTHORS Selvakumar,A., Mohanraj,B.K., Eddy,R.L., Shows,T.B., White,P.C. and  
Dupont,B.  
TITLE Genomic organization and chromosomal location of the human gene  
encoding the B-lymphocyte activation antigen B7  
JOURNAL Immunogenetics 36 (3), 175-181 (1992)  
PUBMED [1377173](#)  
REFERENCE 26 (bases 1 to 2824)  
AUTHORS Freeman,G.J., Freedman,A.S., Segil,J.M., Lee,G., Whitman,J.F. and  
Nadler,L.M.  
TITLE B7, a new member of the Ig superfamily with unique expression on  
activated and neoplastic B cells  
JOURNAL J. Immunol. 143 (8), 2714-2722 (1989)  
PUBMED [2794510](#)  
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Jun 8 2004 17:01:12



# results of BLAST

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**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

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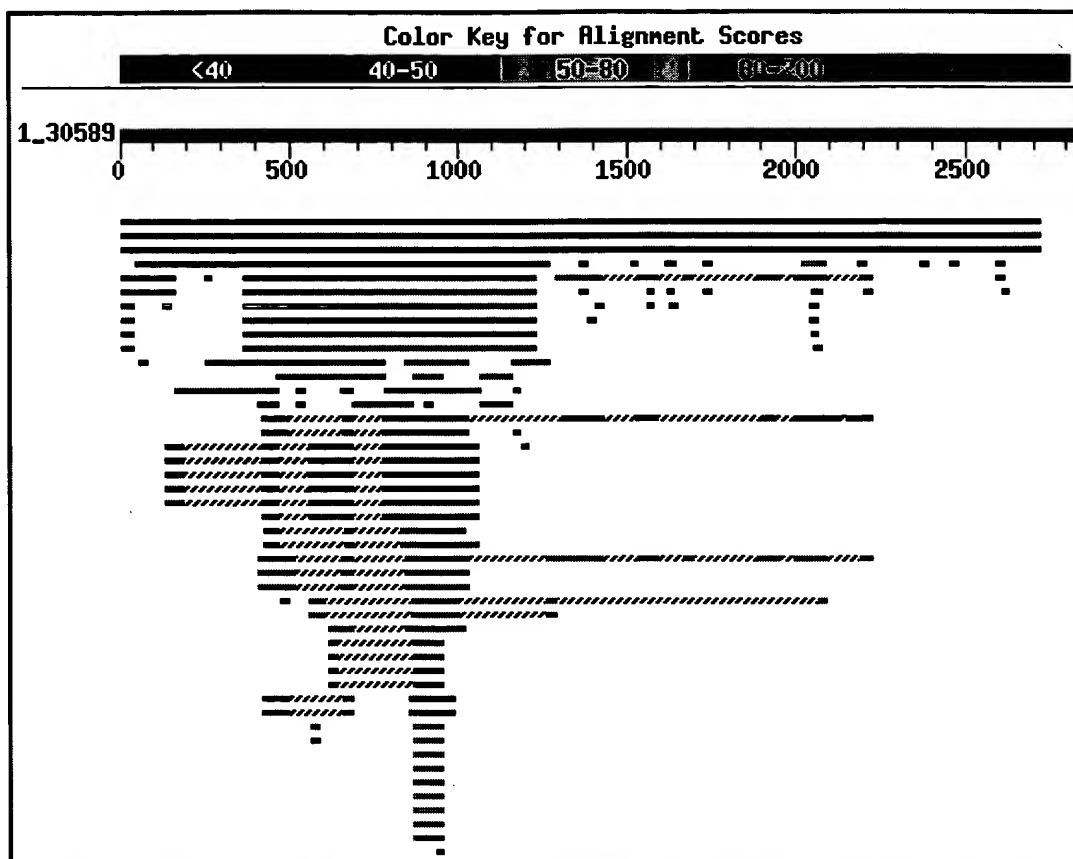
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If you have any problems or questions with the results of this search please refer to the **BLAST FAQs**

Taxonomy reports

## **Distribution of 165 Blast Hits on the Query Sequence**

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gi 644783 gb U19833.1 CTU19833	Cercocebus torquatus B7 prot...	1501	0.0	
gi 22651512 gb AY081815.1	Homo sapiens costimulatory molec...	1027	0.0	U
gi 179324 gb M83073.1 HUMB7AN03	Homo sapiens antigen B7 gen...	634	e-178	
gi 179323 gb M83072.1 HUMB7AN02	Homo sapiens antigen B7 gen...	599	e-167	
gi 179325 gb M83074.1 HUMB7AN04	Homo sapiens antigen B7 gen...	563	e-157	
gi 1262191 gb U33208.1 HSU33208	Human B-lymphocyte activati...	325	3e-85	G
gi 179322 gb M83071.1 HUMB7AN01	Homo sapiens antigen B7 gen...	325	3e-85	
gi 46849851 gb AY591920.1	Macaca fascicularis CD80 mRNA, p...	317	7e-83	
gi 2065520 gb U57755.1 FCU57755	Felis catus T-cell specific...	254	9e-64	
gi 9796385 dbj AB030651.1	Felis catus mRNA for B-lymphocyt...	254	9e-64	
gi 6653506 gb AF203443.1 AF203443	Sus scrofa CD80 protein p...	226	2e-55	LU
gi 6653504 gb AF203442.1 AF203442	Sus scrofa CD80 protein p...	226	2e-55	U
gi 18072036 gb AF455811.1	Sus scrofa CD80 (CD80) mRNA, com...	226	2e-55	LU

gi 8100070 dbj AB038153.2	Sus scrofa mRNA for CD80 protein...	226	2e-55	U
gi 13591561 dbj AB049760.1	Sus scrofa CD80/B7-1 mRNA for C...	226	2e-55	LU
gi 8100061 dbj AB026121.2	Sus scrofa mRNA for CD80 protein...	226	2e-55	U
gi 179327 gb M83077.1 HUMB7AN06	Homo sapiens antigen B7 gen...	220	1e-53	L
gi 22775283 gb AF536987.1	Synthetic construct CD28 binding...	216	2e-52	
gi 2677623 emb Y09950.1 BTCD80	B.taurus CD80 mRNA	202	3e-48	LU
gi 1685044 gb U72535.1 HSU72535	Homo sapiens LIM domain pro...	192	3e-45	L
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gi 7739770 gb AF257653.1 AF257653	Canis familiaris T-cell c...	163	3e-36	U
gi 6572505 gb AF106831.1 CFCD80Y4	Canis familiaris secreted...	163	3e-36	
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gi 6572512 gb AF106824.1 AF106824	Canis familiaris B7-1 pro...	163	3e-36	LU
gi 25188155 dbj AB085743.1	Mesocricetus auratus B7-1b mRNA...	123	2e-24	
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gi 755096 dbj D49843.1 RABCD80C	Oryctolagus cuniculus mRNA ...	101	8e-18	
gi 507872 gb U10925.1 RNU10925	Rattus norvegicus NEDH B7-1 ...	95	5e-16	LUG
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gi 2853280 gb U88622.1 RNU88622	Rattus norvegicus CD80 mRNA...	87	1e-13	LU
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gi 10566942 dbj AB033127.1	Homo sapiens CD80 gene, promote...	81	7e-12	
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gi 46931443 gb AC102091.7	Mus musculus chromosome 18, clon...	46	0.41	
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gi 17537964 ref NM_063761.1	Caenorhabditis elegans general...	42	6.4	LU
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gi 20270106 gb AC106754.3	Homo sapiens chromosome 5 clone ...	42	6.4	
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gi 20146404 dbj AP003792.4	Oryza sativa (japonica cultivar...	42	6.4	
gi 23337491 emb AL805958.8	Mouse DNA sequence from clone R...	42	6.4	
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gi 20068706 emb AL669876.7	Human DNA sequence from clone R...	42	6.4	
gi 20068679 emb AL663033.10	Mouse DNA sequence from clone ...	42	6.4	

## Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|27503575|gb|BC042665.1| LU Homo sapiens CD80 antigen (CD28 antigen ligand 1  
(cDNA clone MGC:34467 IMAGE:5181343), complete cds  
Length = 2824

Score = 5356 bits (2702), Expect = 0.0

Identities = 2716/2723 (99%)

Strand = Plus / Plus

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Identities = 2716/2723 (99%)  
Strand = Plus / Plus

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|||||  
Sbjct: 661 tccattgtgatcctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctg 720

Query: 721 aagtatgaaaaagacgctttcaagcgggaacacctggctgaagtgacgttatcagtcaa 780  
|||||  
Sbjct: 721 aagtatgaaaaagacgctttcaagcgggaacacctggctgaagtgacgttatcagtcaa 780

Query: 781 gctgacttcctacacctagtatatctgactttgaaattccaacttctaataattagaagg 840  
|||||  
Sbjct: 781 gctgacttcctacacctagtatatctgactttgaaattccaacttctaataattagaagg 840

Query: 841 ataatttgctcaacctctggagggttttccagagcctcacctctcctgggttggaatgga 900  
|||||  
Sbjct: 841 ataatttgctcaacctctggagggttttccagagcctcacctctcctgggttggaatgga 900

Query: 901 gaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgct 960  
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Sbjct: 901 gaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgct 960

Query: 961 gtttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaag 1020  
|||||  
Sbjct: 961 gtttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaag 1020

Query: 1021 tatggacatttaagagtgaatcagaccttcaactggaatacaaccaagcaagagcatttt 1080  
|||||  
Sbjct: 1021 tatggacatttaagagtgaatcagaccttcaactggaatacaaccaagcaagagcatttt 1080

Query: 1081 cctgataacctgctcccatcctgggccattaccttaatctcagtaaattggaatTTTTgtg 1140  
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Sbjct: 1081 cctgataacctgctcccatcctgggccattaccttaatctcagtaaattggaatTTTTgtg 1140

Query: 1141 atatgctgcctgacctactgctttgcccccaagatgcagagagagaaggaggaatgagaga 1200  
|||||  
Sbjct: 1141 atatgctgcctgacctactgctttgcccccaagatgcagagagagaaggaggaatgagaga 1200

Query: 1201 ttgagaagggaaagtgtacgccctgtataacagtgtccgcagaagcaaggggctgaaaag 1260  
|||||  
Sbjct: 1201 ttgagaagggaaagtgtacgccctgtataacagtgtccgcagaagcaaggggctgaaaag 1260

Query: 1261 atctgaagggtctcacctccatttgcaattgacctcttctgggaacttcctcagatggaca 1320  
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Sbjct: 1261 atctgaagggtctcacctccatttgcaattgacctcttctgggaacttcctcagatggaca 1320

Query: 1321 agattacccaccttgccctttacgtatctgctcttaggtgcttcttcacttcagttgct 1380  
|||||  
Sbjct: 1321 agattacccaccttgccctttacgtatctgctcttaggtgcttcttcacttcagttgct 1380

Query: 1381 ttgcaggaagtgtctagaggaatatggtgggcacagaagtagctctggtgaccttgatca 1440  
|||||  
Sbjct: 1381 ttgcaggaagtgtctagaggaatatggtgggcacagaagtagctctggtgaccttgatca 1440

Query: 1441 aggggttttgaaatgcagaattcttgagttctggaagggaactttagagaataccagtgtt 1500  
|||||  
Sbjct: 1441 aggggttttgaaatgcagaattcttgagttctggaagggaactttagagaataccagtgtt 1500

Query: 1501 attaatgacaaaggcactgaggcccaggagggtgacccgaattataaaggccagcgccag 1560  
|||||  
Sbjct: 1501 attaatgacaaaggcactgaggcccaggagggtgacccgaattataaaggccagcgccag 1560

Query: 1561 aaccagatttcctaactctggtgctctttccctttatcagtttgactgtggcctgttaa 1620  
|||||  
Sbjct: 1561 aaccagatttcctaactctggtgctctttccctttatcagtttgactgtggcctgttaa 1620

Query: 1621 ctggtatatacatatatatgtcaggcaaagtgtgctggaagtagaatttgtccaataac 1680  
|||||  
Sbjct: 1621 ctggtatatacatatatatgtcaggcaaagtgtgctggaagtagaatttgtccaataac 1680

Query: 1681 aggtcaacttcagagactatctgatttcctaattgtcagagtagaagattttatgctgctg 1740  
|||||  
Sbjct: 1681 aggtcaacttcagagactatctgatttcctaattgtcagagtagaagattttatgctgctg 1740

Query: 1741 tttacaaaagcccaatgtaatgcataggaagtatggcatgaacatctttaggagactaat 1800  
|||||  
Sbjct: 1741 tttacaaaagcccaatgtaatgcataggaagtatggcatgaacatctttaggagactaat 1800

Query: 1801 ggaaatattattggtgtttaccagatttccannnnnnncattgtgttctctattgctgc 1860  
|||||  
Sbjct: 1801 ggaaatattattggtgtttaccagatttccatttttttcattgtgttctctattgctgc 1860

Query: 1861 tctctcactcccccatgaggtacagcagaaaggagaactatccaaaactaatttcctctg 1920  
|||||  
Sbjct: 1861 tctctcactcccccatgaggtacagcagaaaggagaactatccaaaactaatttcctctg 1920

Query: 1921 acatgtaagacgaatgatttaggtacgtcaaagcagtagtcaaggaggaaagggatagtc 1980  
|||||  
Sbjct: 1921 acatgtaagacgaatgatttaggtacgtcaaagcagtagtcaaggaggaaagggatagtc 1980

Query: 1981 caaagacttaactgggtcatattggactgataatctctttaaatggctttatgctagttt 2040  
|||||  
Sbjct: 1981 caaagacttaactgggtcatattggactgataatctctttaaatggctttatgctagttt 2040

Query: 2041 gacctcatttgtaaaatatttatgagaaagttctcatttaaaatgagatcggtgtttaca 2100  
|||||  
Sbjct: 2041 gacctcatttgtaaaatatttatgagaaagttctcatttaaaatgagatcggtgtttaca 2100

Query: 2101 gtgtatgtactaagcagtaagctatcttcaaagtctaaaggtagtaactttccatagggc 2160  
|||||  
Sbjct: 2101 gtgtatgtactaagcagtaagctatcttcaaagtctaaaggtagtaactttccatagggc 2160

Query: 2161 ctcttagatccctaagatggctttttctccttggtatttctgggtctttctgacatcag 2220  
|||||  
Sbjct: 2161 ctcttagatccctaagatggctttttctccttggtatttctgggtctttctgacatcag 2220

Query: 2221 cagagaactggaaagacatagccaactgctgttcattgttactcatgactcctttctctaa 2280  
|||||  
Sbjct: 2221 cagagaactggaaagacatagccaactgctgttcattgttactcatgactcctttctctaa 2280

Query: 2281 aactgccttccacaattcactagaccagaagtggacgcaacttaagctgggataatcaca 2340  
|||||  
Sbjct: 2281 aactgccttccacaattcactagaccagaagtggacgcaacttaagctgggataatcaca 2340

Query: 2341 ttatcatctgaaaatctggagttgaacagcaaaagaagacaacatttctcaaatgcacat 2400  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 2341 ttatcatctgaaaatctggagttgaacagcaaaagaagacaacatttctcaaatgcacat 2400

Query: 2401 ctcatggcagctaagccacatggctgggatttaaagcctttagagccagcccatggcttt 2460  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 2401 ctcatggcagctaagccacatggctgggatttaaagcctttagagccagcccatggcttt 2460

Query: 2461 agctacctcactatgctgcttcacaaaccttgctcctgtgtaaaactatattctcagtgt 2520  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 2461 agctacctcactatgctgcttcacaaaccttgctcctgtgtaaaactatattctcagtgt 2520

Query: 2521 agggcagagaggtctaacaccaacataaggtactagcagtgtttcccgattgacaggaa 2580  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 2521 agggcagagaggtctaacaccaacataaggtactagcagtgtttcccgattgacaggaa 2580

Query: 2581 tacttaactcaataattcttttcttttccatttagtaacagttgtgatgactatgtttct 2640  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 2581 tacttaactcaataattcttttcttttccatttagtaacagttgtgatgactatgtttct 2640

Query: 2641 attctaagtaattcctgtattctacagcagatactttgtcagcaataactaagggaagaaa 2700  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 2641 attctaagtaattcctgtattctacagcagatactttgtcagcaataactaagggaagaaa 2700

Query: 2701 caaagttgaaccgtttctttaat 2723  
 ||||||||||||||||||||  
 Sbjct: 2701 caaagttgaaccgtttctttaat 2723

☐ >gi|19033385|gb|AC073352.22| ☒ Homo sapiens 3 BAC RP11-190C22 (Roswell Park Canc  
 Library) complete sequence  
 Length = 159738

Score = 2831 bits (1428), Expect = 0.0  
 Identities = 1448/1457 (99%)  
 Strand = Plus / Plus

Query: 1267 aggtctcacctccatttgcaattgacctcttctgggaacttctcagatggacaagatta 1326  
 ||||| ||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 116804 aggtcccacctccatttgcaattgacctcttctgggaacttctcagatggacaagatta 116863

Query: 1327 cccaccttgccctttacgtatctgctcttaggtgcttcttcacttcagttgctttgcag 1386  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 116864 cccaccttgccctttacgtatctgctcttaggtgcttcttcacttcagttgctttgcag 116923

Query: 1387 gaagtgtctagaggaatatggtgggcacagaagtagctctggtgaccttgatcaaggggt 1446  
 ||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 116924 gaagtgtctagaggaatatggtgggcacagaagtagctctggtgaccttgatcaaggtgt 116983



Query: 1447     tttgaaatgcagaattcttgagttctggaagggacttttagagaataaccagtgttattaat 1506  
                 |||  
Sbjct: 116984   tttgaaatgcagaattcttgagttctggaagggacttttagagaataaccagtgttattaat 117043

Query: 1507     gacaaaggcactgaggcccagggaggtgacccgaattataaaggccagcgccagaaccca 1566  
                 |||  
Sbjct: 117044   gacaaaggcactgaggcccagggaggtgacccgaattataaaggccagcgccagaaccca 117103

Query: 1567     gatttcctaactctggtgctctttccctttatcagtttgactgtggcctgttaactggta 1626  
                 |||  
Sbjct: 117104   gatttcctaactctggtgctctttccctttatcagtttgactgtggcctgttaactggta 117163

Query: 1627     tatacatatatatgtcaggcaaagtgtgctggaagtagaatttgtccaataacagggtca 1686  
                 |||  
Sbjct: 117164   tatacatatatatgtcaggcaaagtgtgctggaagtagaatttgtccaataacagggtca 117223

Query: 1687     acttcagagactatctgatttcctaattgtcagagtagaagattttatgctgctgtttaca 1746  
                 |||  
Sbjct: 117224   acttcagagactatctgatttcctaattgtcagagtagaagattttatgctgctgtttaca 117283

Query: 1747     aaagcccaatgtaatgcataggaagtatggcatgaacatctttaggagactaatggaaat 1806  
                 |||  
Sbjct: 117284   aaagcccaatgtaatgcataggaagtatggcatgaacatctttaggagactaatggaaat 117343

Query: 1807     attattggtgtttaccagatttccannnnnnncattgtgttctctattgctgctctctc 1866  
                 |||  
Sbjct: 117344   attattggtgtttaccagatttccatttttttcattgtgttctctattgctgctctctc 117403

Query: 1867     actcccccatgaggtacagcagaaaggagaactatccaaaactaatttcctctgacatgt 1926  
                 |||  
Sbjct: 117404   actcccccatgaggtacagcagaaaggagaactatccaaaactaatttcctctgacatgt 117463

Query: 1927     aagacgaatgatttaggtacgtcaaagcagtagtcaaggaggaaagggatagtccaaaga 1986  
                 |||  
Sbjct: 117464   aagacgaatgatttaggtacgtcaaagcagtagtcaaggaggaaagggatagtccaaaga 117523

Query: 1987     cttaactggttcatttggactgataatctctttaaatggctttatgctagtttgacctc 2046  
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Sbjct: 117524   cttaactggttcatttggactgataatctctttaaatggctttatgctagtttgacctc 117583

Query: 2047     atttgtaaaatatttatgagaaagttctcatttaaaatgagatcgttgtttacagtgtat 2106  
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Sbjct: 117584   atttgtaaaatatttatgagaaagttctcatttaaaatgagatcgttgtttacagtgtat 117643

Query: 2107     gtactaagcagtaagctatcttcaaagtgtctaaggtagtaactttccatagggcctcctt 2166  
                 |||  
Sbjct: 117644   gtactaagcagtaagctatcttcaaagtgtctaaggtagtaactttccatagggcctcctt 117703

Query: 2167 agatccctaagatggcctttttctccttggtattttctgggtctttctgacatcagcagaga 2226  
|||||  
Sbjct: 117704 agatccctaagatggcctttttctccttggtattttctgggtctttctgacatcagcagaga 117763

Query: 2227 actggaaagacatagccaactgctgttcatgttactcatgactcctttctctaaaactgc 2286  
|||||  
Sbjct: 117764 actggaaagacatagccaactgctgttcatgttactcatgactcctttctctaaaactgc 117823

Query: 2287 cttccacaattcactagaccagaagtggacgcaacttaagctgggataatcacattatca 2346  
|||||  
Sbjct: 117824 cttccacaattcactagaccagaagtggacgcaacttaagctgggataatcacattatca 117883

Query: 2347 tctgaaaatctggagttgaacagcaaaagaagacaacattttctcaaatgcacatctcatg 2406  
|||||  
Sbjct: 117884 tctgaaaatctggagttgaacagcaaaagaagacaacattttctcaaatgcacatctcatg 117943

Query: 2407 gcagctaagccacatggctgggatttaaagccttttagagccagcccatggcttttagctac 2466  
|||||  
Sbjct: 117944 gcagctaagccacatggctgggatttaaagccttttagagccagcccatggcttttagctac 118003

Query: 2467 ctcactatgctgcttcacaaaccttgctcctgtgtgtaaaactatattctcagtgtagggca 2526  
|||||  
Sbjct: 118004 ctcactatgctgcttcacaaaccttgctcctgtgtgtaaaactatattctcagtgtagggca 118063

Query: 2527 gagaggtctaacaccaacataaggtactagcagtgtttcccgtattgacaggaataactta 2586  
|||||  
Sbjct: 118064 gagaggtctaacaccaacataaggtactagcagtgtttcccgtattgacaggaataactta 118123

Query: 2587 actcaataattcttttcttttccatttagtaacagttgtgatgactatgtttctatttcta 2646  
|||||  
Sbjct: 118124 actcaataattcttttcttttccatttagtaacagttgtgatgactatgtttctatttcta 118183

Query: 2647 agtaattcctgtatttctacagcagatactttgtcagcaataactaaggggaagaaacaaagt 2706  
|||||  
Sbjct: 118184 agtaattcctgtatttctacagcagatactttgtcagcaataactaaggggaagaaacaaagt 118243

Query: 2707 tgaaccgtttctttaat 2723  
|||||  
Sbjct: 118244 tgaaccgtttctttaat 118260

Score = 634 bits (320), Expect = e-178  
Identities = 320/320 (100%)  
Strand = Plus / Plus

Query: 462 aggtgttatccacgtgaccaaggaagtgaagaaagtggcaacgctgtcctgtgggtcaciaa 521  
|||||

Sbjct: 97686 aggtgttatccacgtgaccaaggaagtgaaagaagtggcaacgctgtcctgtggtcacaa 97745

Query: 522 tgtttctgttgaagagctggcaciaactcgcatctactggcaaaaggagaagaaaatggg 581

|||||  
Sbjct: 97746 tgtttctgttgaagagctggcaciaactcgcatctactggcaaaaggagaagaaaatggg 97805

Query: 582 gctgactatgatgtctggggacatgaatatatggcccgagtacaagaaccggaccatctt 641

|||||  
Sbjct: 97806 gctgactatgatgtctggggacatgaatatatggcccgagtacaagaaccggaccatctt 97865

Query: 642 tgatatcactaataacctctccattgtgatcctggctctgcgcccatctgacgagggcac 701

|||||  
Sbjct: 97866 tgatatcactaataacctctccattgtgatcctggctctgcgcccatctgacgagggcac 97925

Query: 702 atacgagtggtgttctgaagtatgaaaaagacgctttcaagcggggaacacctggctga 761

|||||  
Sbjct: 97926 atacgagtggtgttctgaagtatgaaaaagacgctttcaagcggggaacacctggctga 97985

Query: 762 agtgacgttatcagtcaaag 781

|||||  
Sbjct: 97986 agtgacgttatcagtcaaag 98005

Score = 599 bits (302), Expect = e-167

Identities = 302/302 (100%)

Strand = Plus / Plus

Query: 164 gctgtgaaactaaatccacaacctttggagaccaggaacaccctccaatctctgtgtgt 223

|||||  
Sbjct: 84627 gctgtgaaactaaatccacaacctttggagaccaggaacaccctccaatctctgtgtgt 84686

Query: 224 tttgtaaacatcactggaggggtcttctacgtgagcaattggattgtcatcagccctgcct 283

|||||  
Sbjct: 84687 tttgtaaacatcactggaggggtcttctacgtgagcaattggattgtcatcagccctgcct 84746

Query: 284 gttttgcacctgggaagtgccttcttacttgggtccaaattggtggctttcactttt 343

|||||  
Sbjct: 84747 gttttgcacctgggaagtgccttcttacttgggtccaaattggtggctttcactttt 84806

Query: 344 gaccctaagcatctgaagccatggggccacacgagggcaggggaacatcaccatccaagt 403

|||||  
Sbjct: 84807 gaccctaagcatctgaagccatggggccacacgagggcaggggaacatcaccatccaagt 84866

Query: 404 gtccatacctcaatttctttcagctcttgggtgctggctgggtctttctcacttctgttcag 463

|||||  
Sbjct: 84867 gtccatacctcaatttctttcagctcttgggtgctggctgggtctttctcacttctgttcag 84926

Query: 464 gt 465

||  
Sbjct: 84927 gt 84928

Score = 563 bits (284), Expect = e-157  
Identities = 284/284 (100%)  
Strand = Plus / Plus

Query: 780 agctgacttccctacacctagatatctgactttgaaattccaacttctaataattagaag 839  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 105135 agctgacttccctacacctagatatctgactttgaaattccaacttctaataattagaag 105194

Query: 840 gataatttgctcaacctctggagggtttccagagcctcacctctcctgggttgaaaatgg 899  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 105195 gataatttgctcaacctctggagggtttccagagcctcacctctcctgggttgaaaatgg 105254

Query: 900 agaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgc 959  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 105255 agaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgc 105314

Query: 960 tgttagcagcaaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaa 1019  
|||||||||||||||||.||||||||||||||||||||||||||||||||||||||||  
Sbjct: 105315 tgttagcagcaaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaa 105374

Query: 1020 gtatggacatttaagagtgaatcagaccttcaactggaatacaa 1063  
||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 105375 gtatggacatttaagagtgaatcagaccttcaactggaatacaa 105418

Score = 325 bits (164), Expect = 3e-85  
Identities = 164/164 (100%)  
Strand = Plus / Plus

Query: 1 aagtaacagaagttagaaggggaaatgtcgctctctgaagattacccaaagaaaaagtg 60  
||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 82953 aagtaacagaagttagaaggggaaatgtcgctctctgaagattacccaaagaaaaagtg 83012

Query: 61 atttgtcattgctttatagactgtaagaagagaacatctcagaagtggagtcttaccctg 120  
||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 83013 atttgtcattgctttatagactgtaagaagagaacatctcagaagtggagtcttaccctg 83072

Query: 121 aaatcaaaggatttaaagaaaaagtggaatttttcttcagcaag 164  
||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct: 83073 aaatcaaaggatttaaagaaaaagtggaatttttcttcagcaag 83116

Score = 220 bits (111), Expect = 1e-53  
Identities = 111/111 (100%)  
Strand = Plus / Plus

Query: 1160 gctttgcccccaagatgcagagagagaaggaggaatgagagattgagaagggaaagtgtac 1219  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 114714 gctttgcccccaagatgcagagagagaaggaggaatgagagattgagaagggaaagtgtac 114773

Query: 1220 gccctgtataacagtgtccgcagaagcaaggggctgaaaagatctgaaggt 1270  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 114774 gccctgtataacagtgtccgcagaagcaaggggctgaaaagatctgaaggt 114824

Score = 192 bits (97), Expect = 3e-45  
 Identities = 97/97 (100%)  
 Strand = Plus / Plus

Query: 1064 ccaagcaagagcatttttctgataacctgctcccatcctgggccattacctaactcag 1123  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 112618 ccaagcaagagcatttttctgataacctgctcccatcctgggccattacctaactcag 112677

Query: 1124 taaatggaatttttgtgatatgctgcctgacctactg 1160  
 ||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 112678 taaatggaatttttgtgatatgctgcctgacctactg 112714

☐ >gi|184680|gb|M27533.1|HUMIGB7 **LUG** Human Ig rearranged B7 protein mRNA VC1-reg  
 Length = 1491

Score = 2426 bits (1224), Expect = 0.0  
 Identities = 1224/1224 (100%)  
 Strand = Plus / Plus

Query: 47 ccaaagaaaaagtgatttgtcattgctttatagactgtaagaagagaacatctcagaagt 106  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 1 ccaaagaaaaagtgatttgtcattgctttatagactgtaagaagagaacatctcagaagt 60

Query: 107 ggagtcttaccctgaaatcaaaggatttaaagaaaaagtggaatttttcttcagcaagct 166  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 61 ggagtcttaccctgaaatcaaaggatttaaagaaaaagtggaatttttcttcagcaagct 120

Query: 167 gtgaaactaaatccacaacctttggagaccaggaacaccctccaatctctgtgtgtttt 226  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
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☐ >gi|22775285|gb|AF536988.1| Synthetic construct CTLA-4 binding protein precursor  
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 Length = 867

Score = 1556 bits (785), Expect = 0.0  
 Identities = 845/865 (97%)  
 Strand = Plus / Plus

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☐ >gi|3414976|gb|AF079519.1|AF079519 Macaca nemestrina B7 protein (B7) mRNA, compl  
 Length = 867

Score = 1548 bits (781), Expect = 0.0  
 Identities = 844/865 (97%)  
 Strand = Plus / Plus

Query: 364 atggggccacacacggaggcaggggaacatcaccatccaagtgtccatacctcaatttcttt 423  
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Query: 424 cagctcttgggtgctggctggctctttctcacttctgttcaggtgttatccacgtgaccaag 483  
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Sbjct: 61 cagctcttgggtgctggctgtctttctcatttctgttcaggtgttatccacgtgaccaag 120

Query: 484 gaagtgaagaagtggcaacgctgtcctgtgggcacaatgtttctgttgaagagctggca 543  
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Query: 604 atgaatatatggcccagtagacaagaaccggaccatctttgatatacctaataacctctcc 663  
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Sbjct: 241 atgaatatatggcccagtagacaagaaccggaccatctttgatatacagaataacctctcc 300

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Query: 1204 agaagggaagtgtacgccctgtat 1228  
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☐ >gi|13655486|gb|AF344849.1|AF344849 Macaca mulatta CD80 protein precursor (N939)  
Length = 867

Score = 1501 bits (757), Expect = 0.0  
Identities = 838/865 (96%)  
Strand = Plus / Plus

Query: 364 atgggccacacacggaggcaggaacatcacatccaagtgtccatacctcaatttcttt 423  
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Sbjct: 1 atgggccacacacggaggcaggaatatcacatccaagtgtccatacctcaagtcttt 60

Query: 424 cagctcttggtgctggctggtctttctcattctgttcaggtgttatccacgtgaccaag 483  
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Query: 484 gaagtgaagaagtggcaacgctgtcctgtgggcacaatgtttctgttgaagagctggca 543  
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 Sbjct: 841 agaagggaaagtgtacgccctgtat 865

☐ >gi|13649996|gb|AF344839.1|AF344839 Cercopithecus torquatus atys CD80 protein (MnB)  
 Length = 867

Score = 1501 bits (757), Expect = 0.0  
 Identities = 838/865 (96%)  
 Strand = Plus / Plus

Query: 364 atgggccacacacggaggcaggaacatcaccatccaagtgtccatacctcaatttcttt 423  
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Query: 424 cagctcttggtgctggctggtctttctcatttctgttcaggtgttatccacgtgaccaag 483  
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☐ >gi|644797|gb|U19840.1|MMU19840 Macaca mulatta B7 protein (B7) mRNA, complete cc  
Length = 867

Score = 1501 bits (757), Expect = 0.0  
Identities = 838/865 (96%)  
Strand = Plus / Plus

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Sbjct: 841 agaagggaaagtgtacgccctgtat 865

☐ >gi|644783|gb|U19833.1|CTU19833 Cercopithecus torquatus B7 protein (B7) mRNA, parti  
Length = 868

Score = 1501 bits (757), Expect = 0.0  
Identities = 838/865 (96%)  
Strand = Plus / Plus

Query: 364 atgggccacacacggaggcaggggaacatcacatccaagtgtccatacctcaatttcttt 423  
|||||  
Sbjct: 1 atgggccacacacggaggcaggggaatcatcatccaagtgtccatacctcaagttcttt 60

Query: 424 cagctcttggtgctggctggtctttctcattctgttcaggtgttatccacgtgaccaag 483  
|||||  
Sbjct: 61 cagctcttggtgctggctggtctttctcattctgttcaggtgttatccacgtgaccaag 120

Query: 484 gaagtgaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggca 543  
|||||  
Sbjct: 121 gaagtgaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggca 180

Query: 544 caaactcgcatctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggac 603  
|||||  
Sbjct: 181 caaactcgcatctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggac 240

Query: 604 atgaatatatggcccgagtacaagaaccggaccatctttgatatacctaataacctctcc 663  
|||||  
Sbjct: 241 atgaatatatggcccgagtacaagaaccggaccatctttgatatacctaataacctctcc 300

Query: 664 attgtgatcctggctctgcgcccatctgacgagggcacatacagagtgtgttctgaag 723  
|||||  
Sbjct: 301 attgtgattctggctctgcgcccatctgacgagggcacatacagagtgtgttctgaag 360



```

Query: 462 aggtgttatccacgtgaccaaggaagtgaaagaagtggaacgctgtcctgtggtcaca 521
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 102 aggtgttatccacgtgaccaaggaagtgaaagaagtggaacgctgtcctgtggtcaca 161

Query: 522 tgtttctgttgaagagctggcacaaactcgcatctactggcaaaaggagaagaaaatggt 581
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 162 tgtttctgttgaagagctggcacaaactcgcatctactggcaaaaggagaagaaaatggt 221

```



Query: 582 gctgactatgatgtctgtgggacatgaatatatggcccgagtacaagaaccggaccatctt 641  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 222 gctgactatgatgtctgtgggacatgaatatatggcccgagtacaagaaccggaccatctt 281

Query: 642 tgatatcactaataacctctccattgtgatcctggctctgcgcccatctgacgagggcac 701  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 282 tgatatcactaataacctctccattgtgatcctggctctgcgcccatctgacgagggcac 341

Query: 702 atacgagtgtgttgttctgaagtatgaaaaagacgctttcaagcggaacacctggctga 761  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 342 atacgagtgtgttgttctgaagtatgaaaaagacgctttcaagcggaacacctggctga 401

Query: 762 agtgacgttatcagtcaaag 781  
 ||||||||||||||||  
 Sbjct: 402 agtgacgttatcagtcaaag 421

☐ >gi|179323|gb|M83072.1|HUMB7AN02 Homo sapiens antigen B7 gene, exon 2  
 Length = 521

Score = 599 bits (302), Expect = e-167  
 Identities = 302/302 (100%)  
 Strand = Plus / Plus

Query: 164 gctgtgaaactaaatccacaaccttggagaccaggaacaccctccaatctctgtgtgt 223  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 120 gctgtgaaactaaatccacaaccttggagaccaggaacaccctccaatctctgtgtgt 179

Query: 224 tttgtaaaccatcactggagggtcttctacgtgagcaattggattgtcatcagccctgcct 283  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 180 tttgtaaaccatcactggagggtcttctacgtgagcaattggattgtcatcagccctgcct 239

Query: 284 gttttgcacctgggaagtgcctgttacttgggtccaaattgttggttttactttt 343  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 240 gttttgcacctgggaagtgcctgttacttgggtccaaattgttggttttactttt 299

Query: 344 gaccctaagcatctgaagccatgggccacacacggaggcaggggaacatcaccatccaagt 403  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 300 gaccctaagcatctgaagccatgggccacacacggaggcaggggaacatcaccatccaagt 359

Query: 404 gtccatacctcaatttctttcagctcttgggtgctggctgggtctttctcacttctgttcag 463  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Sbjct: 360 gtccatacctcaatttctttcagctcttgggtgctggctgggtctttctcacttctgttcag 419

Query: 464 gt 465  
 ||  
 Sbjct: 420 gt 421

☐ >gi|179325|gb|M83074.1|HUMB7AN04 Homo sapiens antigen B7 gene, exon 4  
Length = 510

Score = 563 bits (284), Expect = e-157  
Identities = 284/284 (100%)  
Strand = Plus / Plus

Query: 780 agctgacttcctacacctagtagtatatctgactttgaaattccaacttctaataattagaag 839  
|||||  
Sbjct: 121 agctgacttcctacacctagtagtatatctgactttgaaattccaacttctaataattagaag 180

Query: 840 gataatttgctcaacctctggagggtttccagagcctcacctctcctgggttgaaaatgg 899  
|||||  
Sbjct: 181 gataatttgctcaacctctggagggtttccagagcctcacctctcctgggttgaaaatgg 240

Query: 900 agaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgc 959  
|||||  
Sbjct: 241 agaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgc 300

Query: 960 tgtttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaa 1019  
|||||  
Sbjct: 301 tgtttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaa 360

Query: 1020 gtatggacatttaagagtgaatcagaccttcaactggaatacaa 1063  
|||||  
Sbjct: 361 gtatggacatttaagagtgaatcagaccttcaactggaatacaa 404

☐ >gi|1262191|gb|U33208.1|HSU33208 ☒ Human B-lymphocyte activation antigen (B7.1)  
and 5' UTR  
Length = 3921

Score = 325 bits (164), Expect = 3e-85  
Identities = 164/164 (100%)  
Strand = Plus / Plus

Query: 1 aagtaacagaagttagaaggggaaatgtcgctctctgaagattacccaaagaaaaagtg 60  
|||||  
Sbjct: 3449 aagtaacagaagttagaaggggaaatgtcgctctctgaagattacccaaagaaaaagtg 3508

Query: 61 atttgtcattgctttatagactgtaagaagagaaacatctcagaagtggagtcttacctg 120  
|||||  
Sbjct: 3509 atttgtcattgctttatagactgtaagaagagaaacatctcagaagtggagtcttacctg 3568

Query: 121 aaatcaaaggatttaagaaaaagtgaatttttcttcagcaag 164  
|||||  
Sbjct: 3569 aaatcaaaggatttaagaaaaagtgaatttttcttcagcaag 3612

☐ >[gi|179322|gb|M83071.1|HUMB7AN01](#) Homo sapiens antigen B7 gene, exon 1  
Length = 374

Score = 325 bits (164), Expect = 3e-85  
Identities = 164/164 (100%)  
Strand = Plus / Plus

Query: 1 aagtaacagaagttagaaggggaaatgtcgcctctctgaagattacccaaagaaaaagtg 60  
|||||  
Sbjct: 110 aagtaacagaagttagaaggggaaatgtcgcctctctgaagattacccaaagaaaaagtg 169

Query: 61 atttgtcattgctttatagactgtaagaagagaacatctcagaagtggagtcttaccctg 120  
|||||  
Sbjct: 170 atttgtcattgctttatagactgtaagaagagaacatctcagaagtggagtcttaccctg 229

Query: 121 aaatcaaaggatttaaagaaaaagtggaatttttcttcagcaag 164  
|||||  
Sbjct: 230 aaatcaaaggatttaaagaaaaagtggaatttttcttcagcaag 273

☐ >[gi|46849851|gb|AY591920.1|](#) Macaca fascicularis CD80 mRNA, partial cds  
Length = 184

Score = 317 bits (160), Expect = 7e-83  
Identities = 178/184 (96%)  
Strand = Plus / Plus

Query: 682 cgcccatctgacgagggcacatacgagtgtgttctgaagtatgaaaaagacgctttc 741  
|||||  
Sbjct: 1 cgcccatctgacgagggcacatacgagtgtgttctgaagtatgaaaaagacgctttc 60

Query: 742 aagcgggaacacctggctgaagtgacgttatcagtc aaagctgacttcctacacctagt 801  
|||||  
Sbjct: 61 aagcgggaacacctggctgaagtgatgttatccgtcaaagctgacttcctacacctagt 120

Query: 802 atatctgactttgaaattccaacttctaataattagaaggataatttgctcaacctctgga 861  
||| |||||  
Sbjct: 121 ataactgactttgaaattccaccttctaacattagaaggataatttgctcaacctctgga 180

Query: 862 gggt 865  
|||  
Sbjct: 181 gggt 184

☐ >[gi|2065520|gb|U57755.1|FCU57755](#) Felis catus T-cell specific surface glycoprotein  
cds  
Length = 941

Score = 254 bits (128), Expect = 9e-64

7/9/2004

Score = 254 bits (128), Expect = 9e-64  
Identities = 221/252 (87%)  
Strand = Plus / Plus

```
Query: 775  gtcaaagctgacttcacctacacctagtataatctgactttgaaattccaacttctaataatt 834
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 620  gtcagagctgacttcacctgtccctagtataaactgatcttggaaatccatctcataacatc 679

Query: 835  agaaggataaatttgctcaacctctggagggttttccagagcctcacctctcctgggttgaa 894
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 680  aaaaggataatgtgcttaacttctggagggttttccaaagcctcacctctcctgggttgaa 739

Query: 895  aatggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctc 954
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 740  aatgaagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctc 799

Query: 955  tatgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcattgtgtctc 1014
          || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 800  tacactattagcagtgaactggatttcaatatgacaacaaccatagcttcctgtgtctt 859

Query: 1015 atcaagtatgga 1026
          ||||| |||||
Sbjct: 860  gtcaagtatgga 871
```

Score = 155 bits (78), Expect = 6e-34  
Identities = 125/138 (90%), Gaps = 2/138 (1%)  
Strand = Plus / Plus

```
Query: 1991 actgggttcatttggactgataatctctttaaattggctttatgctagtttgacctcattt 2050
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1825 actgggttcatttggactgataatctccttaaattggcttcattggt-gtttaacctcattt 1883

Query: 2051 gtaaaatatttatgagaaagttctcattttaaattgagatcggttggttacagtgtatgtac 2110
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1884 ataaaatatttatgagaaagttctcattttaaattgagatagggtttttattgtgtat-tac 1942

Query: 2111 taagcagtaagctatctt 2128
          ||| ||||| |||||
Sbjct: 1943 taaacagtaagctatctt 1960
```

Score = 69.9 bits (35), Expect = 3e-08  
Identities = 56/63 (88%)  
Strand = Plus / Plus

```
Query: 1528 ggagggtgacccgaattataaaggccagcgccagaacccagatttcctaactctgggtgctc 1587
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

7/9/2004

```
Query: 2210 tctgacatcagcagagaa 2227
          ||||| |||||
Sbjct: 2046 tctgagatcagcagagaa 2063
```

Score = 50.1 bits (25), Expect = 0.026  
Identities = 31/33 (93%)  
Strand = Plus / Plus

☐ >[gi|6653506|gb|AF203443.1|AF203443](#) **L****U** Sus scrofa CD80 protein precursor (CD80)  
 Length = 1167

Score = 226 bits (114), Expect = 2e-55  
Identities = 240/282 (85%)  
Strand = Plus / Plus

```

Query: 1015 atcaagtatggacattttaagagtgaatcagaccttcaactgg 1056
          |||||
Sbjct: 941  gtcaagtatggaggcttaacagtgtcacagaccttcaactgg 982

```

7/9/2004

Strand = Plus / Plus

Query: 556 tactggcaaaaggagaagaaaatggtgctgactatgatgtctggggacatgaatatatgg 615  
|||||  
Sbjct: 482 tactggcaaaaggataaatgaaatggtgctggctgtcatgtctggaaaagtgaagggtgtgg 541

Query: 616 cccgagtacaagaaccggaccatctttgatatcactaataacctctccattgtgatcctg 675  
|||  
Sbjct: 542 cccaagtatgagaaccgcaccttcactgatgtcaccaataacctctgcattgtgatcctg 601

Query: 676 gctctgcgcc 685  
|||  
Sbjct: 602 gctctgcgcc 611

Score = 67.9 bits (34), Expect = 1e-07  
Identities = 43/46 (93%)  
Strand = Plus / Plus

Query: 419 tctttcagctcttggtgctggctggtctttctcacttctgttcagg 464  
|||||  
Sbjct: 345 tctttcagctcttggtgctgggtggtctttttgacttctgttcagg 390

Score = 50.1 bits (25), Expect = 0.026  
Identities = 46/53 (86%)  
Strand = Plus / Plus

Query: 137 agaaaaagtggaatttttcttcagcaagctgtgaaactaaatccacaaccttt 189  
|||||  
Sbjct: 57 agaaaaggaggaattattcttcagcaagttgtgaaaataaatctacaatcttt 109

☐ >gi|6653504|gb|AF203442.1|AF203442 ☒ Sus scrofa CD80 protein precursor (CD80) mF  
Length = 1206

Score = 226 bits (114), Expect = 2e-55  
Identities = 240/282 (85%)  
Strand = Plus / Plus

Query: 775 gtcaaagctgacttcctacacctagtatatctgactttgaaattccaacttctaatt 834  
|||||  
Sbjct: 701 gtcaaagctgactttcctgtgcctagtattactgcccttggaatccatctcctaatac 760

Query: 835 agaaggataatttgctcaacctctggagggttttccagagcctcacctctcctgggtggaa 894  
|  
Sbjct: 761 aaaaggataagggtgctcaacctctggagggttttccagagcctcacctctcctgggtggaa 820

Query: 895 aatggagaagaattaaatgccatcaacacaacagtttccaagatcctgaaactgagctc 954



Score = 75.8 bits (38), Expect = 5e-10  
Identities = 107/130 (82%)  
Strand = Plus / Plus

```
Query:  676  gctctgcgcc  685
          |||||
Sbjct:  602  gctctgcgcc  611
```

Score = 67.9 bits (34), Expect = 1e-07  
Identities = 43/46 (93%)  
Strand = Plus / Plus

```

Query:  419  tctttcagctcttgggtgctggctgggtctttctcacttctgttcagg  464
          |||||||
Spbict: 345  tctttcagctcttgggtgctgggtcttttgaacttctgttcagg  390

```

Score = 50.1 bits (25), Expect = 0.026  
Identities = 46/53 (86%)  
Strand = Plus / Plus

```
Query: 137 agaaaaagtggaaattttcttcagcaagctgtgaaactaaatccacaaccttt 189
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbict: 57 agaaaaaggaggaattattcttcagcaagttgtgaaaataaatctacaatcttt 109
```

☐ >gi|18072036|gb|AF455811.1| **LU** Sus scrofa CD80 (CD80) mRNA, complete cds  
 Length = 1112

Score = 226 bits (114), Expect = 2e-55  
Identities = 240/282 (85%)  
Strand = Plus / Plus

Query: 775 gtcaaagctgacttcctacacctagatatctgactttgaaattccaacttctaatt 834  
|||||||  
Sbjct: 397 gtcaaagctgactttcctgtgcctagattactgcccttggaatccatctcctaactc 456

Query: 835 agaaggataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaa 894  
|  
Sbjct: 457 aaaaggataagggtgctcaacctctggaggttttccagagcctcacctctcctggttggaa 516

Query: 895 aatggagaagaattaaatgccatcaacacacagtttcccaagatcctgaaactgagctc 954  
|||||||  
Sbjct: 517 aatggagaagaattaaatgctaccaacacgatgcttcccaagatcctgaaactgagctc 576

Query: 955 tatgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctc 1014  
||  
Sbjct: 577 tacatgattagcagtgaactggatttcaatgtgacaggcaaccacagcttcatgtgtctt 636

Query: 1015 atcaagtatggacatttaagagtgaatcagaccttcaactgg 1056  
|||||||  
Sbjct: 637 gtcaagtatggaggcttaacagtgtcacagaccttcaactgg 678

Score = 75.8 bits (38), Expect = 5e-10  
Identities = 107/130 (82%)  
Strand = Plus / Plus

Query: 556 tactggcaaaaggagaagaaaatggtgctgactatgatgtctggggacatgaatatatgg 615  
|||||||  
Sbjct: 178 tactggcaaaaggataatgaaatggtgctggctgtcatgtctggaaaagtgaaggtgtgg 237

Query: 616 cccgagtacaagaaccggaccatctttgatatcactaataacctctccattgtgatcctg 675  
|||  
Sbjct: 238 cccaagtatgagaaccgcaccttactgatgtcaccaataacctctgcattgtgatcctg 297

Query: 676 gctctgcgcc 685  
|||||||  
Sbjct: 298 gctctgcgcc 307

Score = 60.0 bits (30), Expect = 3e-05  
Identities = 42/46 (91%)  
Strand = Plus / Plus

Query: 419 tctttcagctcttggtgctggctggtctttctcacttctgttcagg 464  
|||||||

Sbjct: 41 tctttcagctcttgggtgccggttggtctttttgacttctgttcagg 86

☐ >gi|8100070|dbj|AB038153.2| ☒ Sus scrofa mRNA for CD80 protein precursor, complete  
Length = 1220

Score = 226 bits (114), Expect = 2e-55  
Identities = 240/282 (85%)  
Strand = Plus / Plus

Query: 775 gtcaaagctgacttcctacacctagtagtatactgactttgaaattccaacttctaataatt 834  
|||||  
Sbjct: 716 gtcaaagctgactttcctgtgcctagtagtattactgcccttggaatccatctcctaataatc 775

Query: 835 agaaggataatttgcctcaacctctggagggttttccagagcctcacctctcctggttgga 894  
|  
Sbjct: 776 aaaaggataaggtgctcaacctctggagggttttccagagcctcacctctcctggttgga 835

Query: 895 aatggagaagaattaaatgccatcaacacaacagtttccaagatcctgaaactgagctc 954  
||  
Sbjct: 836 aatggagaagaattaaatgctaccaacacagatgcttccaagatcctgaaactgagctc 895

Query: 955 tatgctgttagcagcaaaactggatttcaatatgacaaccaaccacagcttcatgtgtctc 1014  
||  
Sbjct: 896 tacatgattagcagtgaactggatttcaatgtgacaggcaaccacagcttcatgtgtctt 955

Query: 1015 atcaagtatggacatttaagagtgaatcagaccttcaactgg 1056  
||  
Sbjct: 956 gtcaagtatggaggcttaacagtgtcacagaccttcaactgg 997

Score = 75.8 bits (38), Expect = 5e-10  
Identities = 107/130 (82%)  
Strand = Plus / Plus

Query: 556 tactggcaaaaggagaagaaaatgggtgctgactatgatgtctggtggacatgaatatatgg 615  
||  
Sbjct: 497 tactggcaaaaggataatgaaatgggtgctggctgtcatgtctggaaaagtgaaggtgtgg 556

Query: 616 cccgagtacaagaaccggaccatctttgatatcactaataacctctccattgtgatcctg 675  
||  
Sbjct: 557 cccaagtatgagaaccgcaccttactgatgtcaccaataacctctgcattgtgatcctg 616

Query: 676 gctctgcgcc 685  
||  
Sbjct: 617 gctctgcgcc 626

Score = 67.9 bits (34), Expect = 1e-07

Identities = 43/46 (93%)  
Strand = Plus / Plus

Query: 419 tctttcagctcttgggtgctggctggctctttctcacttctgttcagg 464  
|||||  
Sbjct: 360 tctttcagctcttgggtgctgggtggctcttttgcacttctgttcagg 405

Score = 42.1 bits (21), Expect = 6.4  
Identities = 45/53 (84%)  
Strand = Plus / Plus

Query: 137 agaaaaagtggaatttttcttcagcaagctgtgaaactaaatccacaaccttt 189  
|||||  
Sbjct: 72 agaaaaggaggaattattcttcagcaagttatgaaaataaatctacaatcttt 124

☐ >gi|13591561|dbj|AB049760.1| **LU** Sus scrofa CD80/B7-1 mRNA for CD80 protein prec  
Length = 2710

Score = 226 bits (114), Expect = 2e-55  
Identities = 240/282 (85%)  
Strand = Plus / Plus

Query: 775 gtcaaagctgacttccctacacctagtatatctgactttgaaattccaacttctaatt 834  
|||||  
Sbjct: 716 gtcaaagctgactttcctgtgcttagtattactgcccttggaatccatctcctaactc 775

Query: 835 agaaggataatttgctcaacctctggagggttttccagagcctcacctctcctggttgaa 894  
|||||  
Sbjct: 776 aaaaggataaggtgctcaacctctggagggttttccagagcctcacctctcctggttgaa 835

Query: 895 aatggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctc 954  
|||||  
Sbjct: 836 aatggagaagaattaaatgctaccaacacagatgctttcccaagatcctgaaactgagctc 895

Query: 955 tatgctgtagcagcaaaactggatttcaatatgacaaccaaccacagcttcatgtgtctc 1014  
||  
Sbjct: 896 tacatgattagcagtgaactggatttcaatgtgacaggcaaccacagcttcatgtgtctt 955

Query: 1015 atcaagtatggacatttaagagtgaatcagaccttcaactgg 1056  
|||||  
Sbjct: 956 gtcaagtatggaggcttaacagtgtcacagaccttcaactgg 997

Score = 75.8 bits (38), Expect = 5e-10  
Identities = 107/130 (82%)  
Strand = Plus / Plus

Query: 556 tactggcaaaaaggagaagaaaatggtgctgactatgatgtctggtgggacatgaatatatgg 615  
|||||||  
Sbjct: 497 tactggcaaaaaggataaatgaaatggtgctggctgtcatgtctggaaaagtgaaggtgtgg 556

Query: 616 cccgagtacaagaaccggaccatctttgatatacctaataacctctccattgtgatcctg 675  
||| ||| ||||| ||| || |||| |||| ||||| ||||| ||||| |||||  
Sbjct: 557 cccaagtatgagaaccgcaccttcactgatgtcaccaataacctctgcattgtgatcctg 616

Query: 676 gctctgcgcc 685  
|||||||  
Sbjct: 617 gctctgcgcc 626

Score = 67.9 bits (34), Expect = 1e-07  
Identities = 43/46 (93%)  
Strand = Plus / Plus

Query: 419 tctttcagctcttgggtgctggctggtctttctcacttctgttcagg 464  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 360 tctttcagctcttgggtgctgggtggtcttttgacttctgttcagg 405

Score = 42.1 bits (21), Expect = 6.4  
Identities = 45/53 (84%)  
Strand = Plus / Plus

Query: 137 agaaaaagtggaatttttcttcagcaagctgtgaaactaaatccacaaccttt 189  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 72 agaaaaggaggaattattcttcagcaagttatgaaaataaatctacaatcttt 124

☐ >gi|8100061|dbj|AB026121.2| ☒ U Sus scrofa mRNA for CD80 protein precursor, complete  
Length = 1189

Score = 226 bits (114), Expect = 2e-55  
Identities = 240/282 (85%)  
Strand = Plus / Plus

Query: 775 gtcaaagctgacttcctacacctagtatatctgactttgaaattccaacttctaatt 834  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 716 gtcaaagctgactttcctgtgcctagtattactgcccttggaatccatctcctaatac 775

Query: 835 agaaggataatttgctcaacctctggagggttttccagagcctcacctctcctggttgga 894  
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 776 aaaaggataaggtgctcaacctctggagggttttccagagcctcacctctcctggttgga 835

Query: 895 aatggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctc 954  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 836 aatggagaagaattaaatgctaccaacacgatgctttcccaagatcctgaaactgagctc 895

```
Query: 1015 atcaagtatggacatttaagagtgaatcagaccttcaactgg 1056
          |||||
Sbjct: 956  gtcaagtatggaggcttaacagtgtcacagaccttcaactgg 997
```

7/9/2004

Strand = Plus / Plus

Query: 1160 gctttgcccccaagatgcagagagagaaggaggaatgagagattgagaagggaaagtgtac 1219  
|||||  
Sbjct: 122 gctttgcccccaagatgcagagagagaaggaggaatgagagattgagaagggaaagtgtac 181

Query: 1220 gccctgtataacagtgtccgcagaagcaaggggctgaaaagatctgaaggt 1270  
|||||  
Sbjct: 182 gccctgtataacagtgtccgcagaagcaaggggctgaaaagatctgaaggt 232

☐ >gi|22775283|gb|AF536987.1| Synthetic construct CD28 binding protein precursor  
complete cds  
Length = 912

Score = 216 bits (109), Expect = 2e-52  
Identities = 172/193 (89%)  
Strand = Plus / Plus

Query: 827 ctaatattagaaggataatttgcacacctctggagggttttccagagcctcacctctcct 886  
|||||  
Sbjct: 473 ctaatatcagaaggctaatttgcacacctctggagggttttccaaggccccacctctact 532

Query: 887 ggttggaataatggagaagaattaaatgccatcaacacacagtttccaagatcctgaaa 946  
|||||  
Sbjct: 533 ggttggaataatggagaagaattaaatgctaccaacacacagtttccaagatcctggaa 592

Query: 947 ctgagctctatgctgtagcagcaaactggatttcaatatgacaaccaaccacagcttca 1006  
|||||  
Sbjct: 593 ctgagctctacatgattagcagtgaactggatttcaatgtgacaataaccacagcatcg 652

Query: 1007 tgtgtctcatcaa 1019  
|||||  
Sbjct: 653 tgtgtctcatcaa 665

Score = 52.0 bits (26), Expect = 0.007  
Identities = 38/42 (90%)  
Strand = Plus / Plus

Query: 423 tcagctcttggtgctggctggtctttctcacttctgttcagg 464  
|||||  
Sbjct: 60 tcagctcttggtgctcactggtcttttttacttctgttcagg 101

Score = 46.1 bits (23), Expect = 0.41  
Identities = 23/23 (100%)  
Strand = Plus / Plus

7/9/2004



exon 5  
Length = 2350

Score = 192 bits (97), Expect = 3e-45  
Identities = 97/97 (100%)  
Strand = Plus / Plus

Query: 1064 ccaagcaagagcattttcctgataacctgctcccatcctgggccattaccttaatctcag 1123  
|||||  
Sbjct: 1835 ccaagcaagagcattttcctgataacctgctcccatcctgggccattaccttaatctcag 1894

Query: 1124 taaatggaatttttgtgatatgctgcctgacctactg 1160  
|||||  
Sbjct: 1895 taaatggaatttttgtgatatgctgcctgacctactg 1931

☐ >gi|179326|gb|M83075.1|HUMB7AN05 Homo sapiens antigen B7 gene, exon 5  
Length = 314

Score = 192 bits (97), Expect = 3e-45  
Identities = 97/97 (100%)  
Strand = Plus / Plus

Query: 1064 ccaagcaagagcattttcctgataacctgctcccatcctgggccattaccttaatctcag 1123  
|||||  
Sbjct: 111 ccaagcaagagcattttcctgataacctgctcccatcctgggccattaccttaatctcag 170

Query: 1124 taaatggaatttttgtgatatgctgcctgacctactg 1160  
|||||  
Sbjct: 171 taaatggaatttttgtgatatgctgcctgacctactg 207

☐ >gi|7739770|gb|AF257653.1|AF257653 ☒ Canis familiaris T-cell co-stimulatory prot  
complete cds  
Length = 972

Score = 163 bits (82), Expect = 3e-36  
Identities = 163/190 (85%)  
Strand = Plus / Plus

Query: 837 aaggataatttgcctcaacctctggagggttttccagagcctcacctctcctgggttgaaaa 896  
|||||  
Sbjct: 500 aaggataatgtgttcaacctctggagggttttccaaagcctcacctctcctgggttgaaaa 559

Query: 897 tggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctcta 956  
|||  
Sbjct: 560 tgaagaagaattgaatgctgccaacacaacagtttcccaagaccggacactgagttgta 619

Query: 957 tgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcattgtgtctcat 1016  
|||  
Sbjct: 560 tgaagaagaattgaatgctgccaacacaacagtttcccaagaccggacactgagttgta 619

Sbjct: 620 cactattagtagtgaactggatttcaatataacaagcaaccatagctttgtgtgtccttgt 679

Query: 1017 caagtatgga 1026

|||||||

Sbjct: 680 caagtatgga 689

Score = 58.0 bits (29), Expect = 1e-04

Identities = 89/109 (81%)

Strand = Plus / Plus

Query: 406 ccatacctcaatttctttcagctcttggtgctggctggtctttctcacttctgttcaggt 465

||||| ||||| ||| |||||||||||||||| ||| ||| | |||||||||||||

Sbjct: 69 ccatactcaaggtctctcagctcttggtgctagctagtctcttttacttctgttcaggc 128

Query: 466 gttatccacgtgaccaaggaagtgaaagaagtggcaacgctgtcctgtg 514

| ||||| |||| |||| |||||||||||| ||| |||||||||

Sbjct: 129 atcatccaggtgaacaagacagtgaaagaagtagcagtactgtcctgtg 177

Score = 46.1 bits (23), Expect = 0.41

Identities = 35/39 (89%)

Strand = Plus / Plus

Query: 647 tcactaataacctctccattgtgatcctggctctgcgcc 685

|||| |||||||||||||| |||| |||||||||

Sbjct: 310 tcaccaataacctctccatcgtagattatggctctgcgcc 348

☐ >[gi|6572505|gb|AF106831.1|CFCD80Y4](#) Canis familiaris secreted B7-1 protein (CD80)  
spliced exon 4 and complete cds  
Length = 1130

Score = 163 bits (82), Expect = 3e-36

Identities = 163/190 (85%)

Strand = Plus / Plus

Query: 837 aaggataatttgctcaacctctggagggttttccagagcctcacctctcctgggtggaaaa 896

||||||| || |||||||||||||||||| ||||||||||||||||| |||||

Sbjct: 262 aaggataatgtgttcaacctctggagggttttccaaagcctcacctctcctgggtggaaaa 321

Query: 897 tggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctcta 956

|| ||||||||| |||| |||||||||||||||||| |||| || ||||| ||

Sbjct: 322 tgaagaagaattgaatgctgccaacacaacagtttcccaagaccggacactgagttgta 381

Query: 957 tgctgtagcagcaaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcat 1016

|| ||||| || |||||||||||||| |||| ||||||| ||||| ||||| ||

Sbjct: 382 cactattagtagtgaactggatttcaatataacaagcaaccatagctttgtgtgtccttgt 441

Query: 1017 caagtatgga 1026  
 |||||  
 Sbjct: 442 caagtatgga 451

☐ >gi|6572514|gb|AF106825.1|AF106825 ☒ Canis familiaris secreted B7-1 protein prec  
 complete cds  
 Length = 1024

Score = 163 bits (82), Expect = 3e-36  
 Identities = 163/190 (85%)  
 Strand = Plus / Plus

Query: 837 aaggataatttgctcaacctctggagggttttccagagcctcacctctcctgggtggaaaa 896  
 |||||  
 Sbjct: 552 aaggataatgtgttcaacctctggagggttttccaaagcctcacctctcctgggtggaaaa 611

Query: 897 tggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctcta 956  
 || |||||  
 Sbjct: 612 tgaagaagaattgaatgctgccaacacaacagtttcccaagaccgacactgagttgta 671

Query: 957 tgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcat 1016  
 || |||||  
 Sbjct: 672 cactattagtagtgaactggatttcaatataacaagcaaccatagctttgtgtgtcttgt 731

Query: 1017 caagtatgga 1026  
 |||||  
 Sbjct: 732 caagtatgga 741

Score = 58.0 bits (29), Expect = 1e-04  
 Identities = 89/109 (81%)  
 Strand = Plus / Plus

Query: 406 ccatacctcaatttctttcagctcttggtgctggctggtctttctcacttctgttcaggt 465  
 |||||  
 Sbjct: 121 ccatactcaaggtctctcagctcttggtgctagctagtctcttttacttctgttcaggc 180

Query: 466 gttatccacgtgaccaaggaagtgaaagaagtggcaacgctgtcctgtg 514  
 | |||||  
 Sbjct: 181 atcatccaggtgaacaagacagtgaaagaagtagcagtactgtcctgtg 229

Score = 46.1 bits (23), Expect = 0.41  
 Identities = 35/39 (89%)  
 Strand = Plus / Plus

Query: 647 tcactaataacctctccattgtgatcctggctctgcgcc 685  
 |||||  
 Sbjct: 362 tcaccaataacctctccatcgtgattatggctctgcgcc 400

☐ >gi|6572512|gb|AF106824.1|AF106824 **LU** Canis familiaris B7-1 protein precursor  
Length = 2830

Score = 163 bits (82), Expect = 3e-36  
Identities = 163/190 (85%)  
Strand = Plus / Plus

```
Query: 837  aaggataatttgctcaacctctggagggttttccagagcctcacctctcctggttgaaaa 896
          ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 810  aaggataatgtgttcaacctctggagggttttccaaagcctcacctctcctggtggaaaa 869

Query: 897  tggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctcta 956
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 870  tgaagaagaattgaatgctgccaacacaacagtttcccaagacccggacactgagttgta 929

Query: 957  tgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcat 1016
          || |||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 930  cactattagtagtgaactggatttcaatataacaagcaaccatagctttgtgtgtcttgt 989

Query: 1017 caagtatgga 1026
          ||||| |||||
Sbjct: 990  caagtatgga 999
```

Score = 107 bits (54), Expect = 1e-19  
Identities = 89/99 (89%), Gaps = 5/99 (5%)  
Strand = Plus / Plus

```
Query: 1991 actgggtcatattggactgataatctctttaaagtggctttatgctagtttgacctcattt 2050
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1986 actgggtcatattggactgataatctcctt-aatggctttatgctagttttaaactcattt 2044

Query: 2051 gtaaaatatttatgagaaagttctcattttaaagtgat 2089
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 2045 ataaaa----catgagaaagttctcattttaaagtgat 2079
```

Score = 77.8 bits (39), Expect = 1e-10  
Identities = 136/167 (81%), Gaps = 1/167 (0%)  
Strand = Plus / Plus

```
Query: 1261 atctgaagggtctcacctccatttgcaattgacctcttctgggaacttcctcagatggaca 1320
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1259 atctggagggtcccacctccatcttagattgacctcatcttgaatttcctcagatggcca 1318

Query: 1321 agattacccaccttgccctttacgtatctgctct-taggtgcttcttcacttcagttgc 1379
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Sbjct: 1379 cctgcagaaagtgaccagaggaatatggtggggacataagtagctct 1425

Strand = Plus / Plus

Sbjct: 379 ccataatctcaaggtctctcagctcttggtgctagctagtctcttttacttctgttcaggc 438

Sbjct: 439 atcatccaggtgaacaagacagtgaaagaagtagcagtactgtcctgtg 487

Strand = Plus / Plus

Sbjct: 1871 agaaagtagatctatccaaaactaatatctgctgacatgtaagatgaatgacttatatac 1930

Sbjct: 1931 ctcaaagc 1938

Strand = Plus / Plus

Sbjct: 2199 ctcccttggtattttctga-tccttctgacatcagcagagaa 2237

Strand = Plus / Plus

Sbjct: 1518 ggtgacctgaatgataaagggtctgagctagaaccagatttcctgtctcgggtgctcttt 1577

Score = 46.1 bits (23), Expect = 0.41  
Identities = 35/39 (89%)  
Strand = Plus / Plus

Query: 647 tcactaataacctctccattgtgatcctggctctgcgcc 685  
||||| ||||||||| ||||| |||||||||  
Sbjct: 620 tcaccaataacctctccatcgatgattatggctctgcgcc 658

Score = 42.1 bits (21), Expect = 6.4  
Identities = 27/29 (93%)  
Strand = Plus / Plus

Query: 1670 tgtccaataacaggtcaacttcagagact 1698  
||||||| ||||||||| |||||||||  
Sbjct: 1659 tgtccaatgtcaggtcaacttcagagact 1687

☐ >gi|25188155|dbj|AB085743.1| Mesocricetus auratus B7-1b mRNA for B7-1, complete  
Length = 2071

Score = 123 bits (62), Expect = 2e-24  
Identities = 125/146 (85%)  
Strand = Plus / Plus

Query: 856 tctggaggttttccagagcctcacctctcctggttggaatggagaagaattaaatgcc 915  
||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||  
Sbjct: 785 tctggaggtttccagagcctcgctcacctggttggaagatggaaaagaattaagcggc 844

Query: 916 atcaacacaacagtttcccaagatcctgaaactgagctctatgctgttagcagcaaactg 975  
||||| ||||| ||||| || ||||||||| ||||| || || ||||| ||  
Sbjct: 845 atcaatacaacaatttctcaggatcctgaatctgaactgtacactgtcagtagcaaactg 904

Query: 976 gatttcaatatgacaaccaaccacag 1001  
||||||| |||||||||  
Sbjct: 905 gatttcaatatgacatacaaccacag 930

Score = 48.1 bits (24), Expect = 0.10  
Identities = 45/52 (86%)  
Strand = Plus / Plus

Query: 553 atctactggcaaaaaggagaagaaaatggtgctgactatgatgtctggggaca 604  
||||||| ||||| || || ||||||||| || || || |||||||||  
Sbjct: 482 atctactggcaaaaagataaggaaaatggtgctgagtttcatctctggggaca 533

Score = 44.1 bits (22), Expect = 1.6  
Identities = 25/26 (96%)  
Strand = Plus / Plus

Query: 1262 tctgaaggtctcacctccatttgcaa 1287  
|||||  
Sbjct: 1170 tctgaaggtctcacctacatttgcaa 1195

☐ >gi|25188153|dbj|AB085742.1| Mesocricetus auratus B7-1a mRNA for B7-1, complete  
Length = 3096

Score = 123 bits (62), Expect = 2e-24  
Identities = 125/146 (85%)  
Strand = Plus / Plus

Query: 856 tctggaggtttccagagcctcacctctcctggttggaaaatggagaagaattaaatgcc 915  
|||||  
Sbjct: 786 tctggaggtttccagagcctcgctcacctggttggaagatggaaaagaattaagcggc 845

Query: 916 atcaacacaacagtttcccaagatcctgaaactgagctctatgctgttagcagcaaactg 975  
|||||  
Sbjct: 846 atcaatacaacaattttctcaggatcctgaatctgaactgtacactgtcagtagcaaactg 905

Query: 976 gatttcaatatgacaaccaaccacag 1001  
|||||  
Sbjct: 906 gatttcaatatgacatacaaccacag 931

Score = 52.0 bits (26), Expect = 0.007  
Identities = 26/26 (100%)  
Strand = Plus / Plus

Query: 2063 tgagaaagttctcattttaaagaga 2088  
|||||  
Sbjct: 2257 tgagaaagttctcattttaaagaga 2282

Score = 48.1 bits (24), Expect = 0.10  
Identities = 45/52 (86%)  
Strand = Plus / Plus

Query: 553 atctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggaca 604  
|||||  
Sbjct: 483 atctactggcaaaaagataaggaaaatggtgctgagtttcatctctggggaca 534

Score = 44.1 bits (22), Expect = 1.6  
Identities = 25/26 (96%)  
Strand = Plus / Plus

Query: 1262 tctgaaggtctcacctccatttgcaa 1287  
 |||  
 Sbjct: 1171 tctgaaggtctcacctacatttgcaa 1196

☐ >gi|6572508|gb|AF106834.1|CFCD80Y7 **G** Canis familiaris B7-1 protein (CD80) gene,  
 Length = 2242

Score = 107 bits (54), Expect = 1e-19  
 Identities = 89/99 (89%), Gaps = 5/99 (5%)  
 Strand = Plus / Plus

Query: 1991 actggttcatttggactgataatctctttaaaggctttatgctagtttgacctcattt 2050  
 |||  
 Sbjct: 1092 actggttcatttggactgataatctcctt-aatggctttatgctagttttaaactcattt 1150

Query: 2051 gtaaaatatttatgagaaagttctcattttaaagat 2089  
 |||  
 Sbjct: 1151 ataaaa----catgagaaagttctcattttaaagat 1185

Score = 73.8 bits (37), Expect = 2e-09  
 Identities = 116/141 (82%), Gaps = 1/141 (0%)  
 Strand = Plus / Plus

Query: 1287 attgacctcttctgggaacttcctcagatggacaagattacccaccttgccctttacgt 1346  
 |||  
 Sbjct: 391 attgacctcatcttgaatttcctcagatggccaggattatccaccttgccctttacgt 450

Query: 1347 atctgctct-taggtgcttcttctcacttcagttgctttgcaggaagtgtctagaggaatat 1405  
 |||  
 Sbjct: 451 atctgttctctaggagcctgttcatttcagttgctttgcaggaagtgtctagaggaatat 510

Query: 1406 ggtgggcacagaagtagctct 1426  
 |||  
 Sbjct: 511 ggtggggacataagtagctct 531

Score = 56.0 bits (28), Expect = 4e-04  
 Identities = 58/68 (85%)  
 Strand = Plus / Plus

Query: 1887 agaaaggagaactatccaaaactaatttcctctgacatgtaagacgaatgatttaggtac 1946  
 |||  
 Sbjct: 977 agaaagtagatctatccaaaactaatttcctctgacatgtaagatgaatgacttatatac 1036

Query: 1947 gtcaaagc 1954  
 |||



Sbjct: 1037 ctcaaagc 1044

Score = 48.1 bits (24), Expect = 0.10  
Identities = 37/40 (92%), Gaps = 1/40 (2%)  
Strand = Plus / Plus

Query: 2188 ctccttggtattttctgggtctttctgacatcagcagagaa 2227  
|||||  
Sbjct: 1305 ctccttggtattttctga-tccttctgacatcagcagagaa 1343

Score = 48.1 bits (24), Expect = 0.10  
Identities = 51/60 (85%)  
Strand = Plus / Plus

Query: 1531 ggtgacccgaattataaaggccagcgccagaaccagatttcctaactctgggtgctcttt 1590  
|||||  
Sbjct: 624 ggtgacctgaatgataaaggctctgagctagaaccagatttcctgtctcgggtgctcttt 683

Score = 42.1 bits (21), Expect = 6.4  
Identities = 27/29 (93%)  
Strand = Plus / Plus

Query: 1670 tgtccaataacagggtcaacttcagagact 1698  
|||||  
Sbjct: 765 tgtccaatgtcagggtcaacttcagagact 793

☐ >gi|755096|dbj|D49843.1|RABCD80C Oryctolagus cuniculus mRNA for CD80, complete c  
Length = 950

Score = 101 bits (51), Expect = 8e-18  
Identities = 150/183 (81%)  
Strand = Plus / Plus

Query: 837 aaggataatttgctcaacctctggagggttttccagagcctcacctctcctgggttgaaaa 896  
|||||  
Sbjct: 492 aaggataagatgctccgcctctggagggttttccagagcctcgccctgcctggatggaaga 551

Query: 897 tggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctcta 956  
|||||  
Sbjct: 552 tggagaagaactaaacgccgtcaacacgacggttgaccaggatttggacacggagctcta 611

Query: 957 tgctgttagcagcaaaactggattttcaatatgacaaccaaccacagcttcattgtgtctcat 1016  
||  
Sbjct: 612 cagcgtcagcagtgaaactggattttcaatgtgacaaataaccacagcatcgtgtgtctcat 671

Query: 1017 caa 1019  
|||  
Sbjct: 672 caa 674

Score = 50.1 bits (25), Expect = 0.026  
Identities = 61/73 (83%)  
Strand = Plus / Plus

Query: 613 tggcccgagtacaagaaccggaccatctttgatatacctaataacctctccattgtgatc 672  
||||| ||||||||| ||| || || ||| ||| ||||||||| ||| |||  
Sbjct: 268 tggcctgagtacaagaaccgcaccttccccgacatcattaacaacctctcccttatgatc 327

Query: 673 ctggctctgcgcc 685  
||||| |||||||  
Sbjct: 328 ctggcactgcgcc 340

☐ >gi|507872|gb|U10925.1|RNU10925 **LUG** Rattus norvegicus NEDH B7-1 (B7-1) mRNA, I  
Length = 1152

Score = 95.6 bits (48), Expect = 5e-16  
Identities = 81/92 (88%)  
Strand = Plus / Plus

Query: 862 ggttttccagagcctcacctctcctggttggaaaatggagaagaattaaatgccatcaac 921  
||||| ||| ||||||| ||||||| ||||||||| ||||||||| ||||||||| |||  
Sbjct: 795 ggtttcccaaagcctcgctctcttggttggaaaatggaagagaattaaatggcatcaat 854

Query: 922 acaacagtttcccaagatcctgaaactgagct 953  
||||| ||||||| ||||||| |||||||  
Sbjct: 855 acaacaatttccaggatcctgaatctgagct 886

Score = 46.1 bits (23), Expect = 0.41  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 613 tggcccgagtacaagaaccggac 635  
||||| ||||||||| |||||||||  
Sbjct: 546 tggcccgagtacaagaaccggac 568

☐ >gi|453381|gb|U05593.1|RRU05593 **LUG** Rattus norvegicus B7-1 mRNA, complete cds  
Length = 1030

Score = 95.6 bits (48), Expect = 5e-16  
Identities = 81/92 (88%)  
Strand = Plus / Plus

Query: 862 ggttttccagagcctcacctctcctggttggaaaatggagaagaattaaatgccatcaac 921  
||||| ||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
Sbjct: 532 ggtttcccaaagcctcgctctcttggttggaaaatggaagagaattaaatggcatcaat 591

Query: 922 acaacagtttcccaagatcctgaaactgagct 953  
||||| ||||||| ||||||| |||||||  
Sbjct: 592 acaacaatttcccaggatcctgaatctgagct 623

☐ >gi|29789033|ref|NM\_012926.1| **LU** Rattus norvegicus CD80 antigen (Cd80), mRNA  
Length = 1000

Score = 87.7 bits (44), Expect = 1e-13  
Identities = 80/92 (86%)  
Strand = Plus / Plus

Query: 862 ggttttccagagcctcacctctcctggttggaaaatggagaagaattaaatgccatcaac 921  
||||| ||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||| ||  
Sbjct: 521 ggtttcccaaagcctcgctctcttggttggaaaatggaagagaattaaatggcattaat 580

Query: 922 acaacagtttcccaagatcctgaaactgagct 953  
||||| ||||||| ||||||| |||||||  
Sbjct: 581 acaacaatttcccaggatcctgaatctgagct 612

Score = 46.1 bits (23), Expect = 0.41  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 613 tggcccagagtacaagaaccggac 635  
||||||| |||||||  
Sbjct: 272 tggcccagagtacaagaaccggac 294

☐ >gi|2317781|gb|AF010465.1|AF010465 **LUG** Rattus norvegicus B7.1 (B7.1) mRNA, con  
Length = 1000

Score = 87.7 bits (44), Expect = 1e-13  
Identities = 80/92 (86%)  
Strand = Plus / Plus

Query: 862 ggttttccagagcctcacctctcctggttggaaaatggagaagaattaaatgccatcaac 921  
||||| ||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||| ||  
Sbjct: 521 ggtttcccaaagcctcgctctcttggttggaaaatggaagagaattaaatggcattaat 580

Query: 922 acaacagtttcccaagatcctgaaactgagct 953  
||||| ||||||| ||||||| |||||||  
Sbjct: 581 acaacaatttcccaggatcctgaatctgagct 612

Score = 46.1 bits (23), Expect = 0.41  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 613 tggcccgagtacaagaaccggac 635  
          |||||  
Sbjct: 272 tggcccgagtacaagaaccggac 294

☐ >gi|2853280|gb|U88622.1|RNU88622 **LU** Rattus norvegicus CD80 mRNA, complete cds  
          Length = 966

Score = 87.7 bits (44), Expect = 1e-13  
Identities = 80/92 (86%)  
Strand = Plus / Plus

Query: 862 ggttttccagagcctcacctctcctggttggaaaatggagaagaattaaatgccatcaac 921  
          ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 514 ggtttcccaaagcctcggctctcctggttggaaaatggaagagaattaaatggcatcaat 573

Query: 922 acaacagtttcccaagatcctgaaactgagct 953  
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 574 acaacaatttccagatcctgaatctgagct 605

Score = 46.1 bits (23), Expect = 0.41  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 613 tggcccgagtacaagaaccggac 635  
          |||||  
Sbjct: 265 tggcccgagtacaagaaccggac 287

☐ >gi|30268719|gb|AF387763.1| Meriones unguiculatus costimulatory molecule B7.1 mRNA  
          cds  
          Length = 1014

Score = 83.8 bits (42), Expect = 2e-12  
Identities = 113/134 (84%), Gaps = 2/134 (1%)  
Strand = Plus / Plus

Query: 852 aacctctggaggttttccagagcctcacctctcct-ggttggaaaatggagaagaattaa 910  
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 496 aacctctggaggtttccagagcctcgc-tctcttggttggaaagtggaagagaattaa 554

Query: 911 atgccatcaacacaacagtttcccaagatcctgaaactgagctctatgctgttagcagca 970  
          | ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 555 ggggcacatcaatacaaccggtttcccaggaccctgaatctgaactgtatgccgtcagtagca 614

Query: 971 aactggatttcaat 984

||||||||||||

Sbjct: 615 aactggatttcaat 628

☐ >gi|37903875|gb|AY223679.1| Meriones unguiculatus costimulatory molecule B7.1 mRNA  
cds  
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Score = 83.8 bits (42), Expect = 2e-12  
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Strand = Plus / Plus

Query: 852 aacctctggaggttttccagagcctcacctctcct-gggttgaaaatggagaagaattaa 910

|||||||||||| |||||||||| ||| |||||||||| ||| ||||||||||

Sbjct: 495 aacctctggaggtttcccagagcctcgc-tctcttgggttgaaagtggaagagaattaa 553

Query: 911 atgccatcaacacaacagtttcccaagatcctgaaactgagctctatgctgttagcagca 970

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Sbjct: 554 ggggcacatcaatacaaccggtttcccaggaccctgaatctgaactgtatgccgtcagtagca 613

Query: 971 aactggatttcaat 984

||||||||||||

Sbjct: 614 aactggatttcaat 627

☐ >gi|10566942|dbj|AB033127.1| Homo sapiens CD80 gene, promoter region, allele:ATG  
Length = 695

Score = 81.8 bits (41), Expect = 7e-12  
Identities = 41/41 (100%)  
Strand = Plus / Plus

Query: 1 aagtaacagaagttagaaggggaaatgtcgccctctctgaag 41

|||||||||||| |||||||||| |||||||||| |||||||||| ||||||||||

Sbjct: 655 aagtaacagaagttagaaggggaaatgtcgccctctctgaag 695

☐ >gi|10566941|dbj|AB033126.1| Homo sapiens CD80 gene, promoter region, allele:CTC  
Length = 690

Score = 81.8 bits (41), Expect = 7e-12  
Identities = 41/41 (100%)  
Strand = Plus / Plus

Query: 1 aagtaacagaagttagaaggggaaatgtcgccctctctgaag 41

|||||||||||| |||||||||| |||||||||| |||||||||| ||||||||||

Sbjct: 650 aagtaacagaagttagaaggggaaatgtcgccctctctgaag 690

☐ >gi|10566940|dbj|AB033125.1| Homo sapiens CD80 gene, promoter region, allele:CCG  
Length = 690

Score = 81.8 bits (41), Expect = 7e-12  
Identities = 41/41 (100%)  
Strand = Plus / Plus

Query: 1 aagtaacagaagttagaaggggaaatgtcgctctctgaag 41  
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Sbjct: 650 aagtaacagaagttagaaggggaaatgtcgctctctgaag 690

☐ >gi|10566939|dbj|AB033124.1| Homo sapiens CD80 gene, promoter region, allele:CTC  
Length = 690

Score = 81.8 bits (41), Expect = 7e-12  
Identities = 41/41 (100%)  
Strand = Plus / Plus

Query: 1 aagtaacagaagttagaaggggaaatgtcgctctctgaag 41  
|||||  
Sbjct: 650 aagtaacagaagttagaaggggaaatgtcgctctctgaag 690

☐ >gi|47084437|gb|AC107274.11| ☒ Rattus norvegicus 18 BAC CH230-207M17 (Children's  
Research Institute) complete sequence  
Length = 217066

Score = 75.8 bits (38), Expect = 5e-10  
Identities = 62/70 (88%)  
Strand = Plus / Minus

Query: 2017 cttttaaaggctttatgctagtttgacctcatttgtaaaatatttatgagaaagttctca 2076  
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Query: 2077 tttaaaatga 2086  
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Sbjct: 171217 tttaaaatga 171208

Get selected sequences

Select all

Deselect all

Lambda K H  
1.37 0.711 1.31

## Gapped

Lambda	K	H
1.37	0.711	1.31

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 2280493

Number of Hits to DB: 35,079,557

Number of extensions: 2029161

Number of successful extensions: 17426

Number of sequences better than 10.0: 25

Number of HSP's better than 10.0 without gapping: 25

Number of HSP's gapped: 17408

Number of HSP's successfully gapped: 42

Number of extra gapped extensions for HSPs above 10.0: 17343

Length of query: 2824

Length of database: 11,051,402,435

Length adjustment: 23

Effective length of query: 2801

Effective length of database: 10,998,951,096

Effective search space: 30808062019896

Effective search space used: 30808062019896

A: 0

X1: 11 (21.8 bits)

X2: 15 (30.0 bits)

X3: 25 (50.0 bits)

S1: 12 (25.0 bits)

S2: 21 (42.1 bits)





- REFERENCE 5 (bases 1 to 2781)  
AUTHORS Fillion,L.G., Matusевич,D., Graziani-Bowering,G.M., Kumar,A. and Freedman,M.S.  
TITLE Monocyte-derived IL12, CD86 (B7-2) and CD40L expression in relapsing and progressive multiple sclerosis  
JOURNAL Clin. Immunol. 106 (2), 127-138 (2003)  
PUBMED [12672403](#)  
REMARK GeneRIF: A key mechanism in the pathogenesis of MS is the increased expression of CD86 and CD40L and the increased production of IL12 during disease progression.
- REFERENCE 6 (bases 1 to 2781)  
AUTHORS Verbovetski,I., Bychkov,H., Trahtenberg,U., Shapira,I., Hareuveni,M., Ben-Tal,O., Kutikov,I., Gill,O. and Mevorach,D.  
TITLE Opsonization of apoptotic cells by autologous iC3b facilitates clearance by immature dendritic cells, down-regulates DR and CD86, and up-regulates CC chemokine receptor 7  
JOURNAL J. Exp. Med. 196 (12), 1553-1561 (2002)  
PUBMED [12486098](#)  
REMARK GeneRIF: Data show that interaction between iC3b-opsonized apoptotic cells and immature dendritic cells down-regulated the expression of CD86 and up-regulated expression of CC chemokine receptor 7.
- REFERENCE 7 (bases 1 to 2781)  
AUTHORS Ke,X.Y., Gribben,J., Wang,J. and Wang,D.B.  
TITLE The identical effects of B7-1 and B7-2 on regulation of human IL-2 gene transcription factors NF-kappa B and AP-1  
JOURNAL Zhongguo Shi Yan Xue Ye Xue Za Zhi 10 (6), 512-518 (2002)  
PUBMED [12513711](#)  
REMARK GeneRIF: The identical effects of B7-1 and B7-2 on regulation of human IL-2 gene transcription factors NF-kappa B and AP-1.
- REFERENCE 8 (bases 1 to 2781)  
AUTHORS Shah,R., Banks,K., Patel,A., Dogra,S., Terrell,R., Powers,P.A., Fenton,C., Dinauer,C.A., Tuttle,R.M. and Francis,G.L.  
TITLE Intense expression of the b7-2 antigen presentation coactivator is an unfavorable prognostic indicator for differentiated thyroid carcinoma of children and adolescents  
JOURNAL J. Clin. Endocrinol. Metab. 87 (9), 4391-4397 (2002)  
PUBMED [12213904](#)  
REMARK GeneRIF: Intense expression is an unfavorable prognostic indicator for differentiated thyroid carcinoma of children and adolescents
- REFERENCE 9 (bases 1 to 2781)  
AUTHORS Venuprasad,K., Banerjee,P.P., Chattopadhyay,S., Sharma,S., Pal,S., Parab,P.B., Mitra,D. and Saha,B.  
TITLE Human neutrophil-expressed CD28 interacts with macrophage B7 to induce phosphatidylinositol 3-kinase-dependent IFN-gamma secretion and restriction of Leishmania growth  
JOURNAL J. Immunol. 169 (2), 920-928 (2002)  
PUBMED [12097397](#)  
REMARK GeneRIF: Leishmania major infection of macrophages cocultured with neutrophils results in a neutrophil-macrophage interaction via CD86 leading to IFN-gamma secretion and restriction of Leishmania growth.
- REFERENCE 10 (bases 1 to 2781)  
AUTHORS Turpeinen,H., Laine,A.P., Nejentsev,S., Sjoroos,M., Ilonen,J., Simell,O., Veijola,R., Knip,M., Akerblom,H.K. and Knip,M.  
TITLE CD86 gene polymorphisms: no association with Type I diabetes among Finnish subjects  
JOURNAL Diabetologia 45 (7), 1041-1042 (2002)  
PUBMED [12187923](#)  
REMARK GeneRIF: polymorphisms have no association with type I diabetes

among Finnish subjects

REFERENCE 11 (bases 1 to 2781)

AUTHORS Groth,C., Drager,R., Warnatz,K., Wolff-Vorbeck,G., Schmidt,S., Eibel,H., Schlesier,M. and Peter,H.H.

TITLE Impaired up-regulation of CD70 and CD86 in naive (CD27-) B cells from patients with common variable immunodeficiency (CVID)

JOURNAL Clin. Exp. Immunol. 129 (1), 133-139 (2002)

PUBMED [12100033](#)

REMARK GeneRIF: Impaired up-regulation of CD70 and CD86 in naive B cells from patients with CVID suggests an intrinsic signalling or expression defect at the level of naive B cells in type I CVID.

REFERENCE 12 (bases 1 to 2781)

AUTHORS Zhang,X., Schwartz,J.C., Almo,S.C. and Nathenson,S.G.

TITLE Expression, refolding, purification, molecular characterization, crystallization, and preliminary X-ray analysis of the receptor binding domain of human B7-2

JOURNAL Protein Expr. Purif. 25 (1), 105-113 (2002)

PUBMED [12071705](#)

REMARK GeneRIF: expression, refolding, purification, characterization, and crystallization of the receptor-binding domain of human B7-2 is described; glycosylation is not important for proper folding of the receptor-binding domain of B7-2 nor for its binding to CTLA-4

REFERENCE 13 (bases 1 to 2781)

AUTHORS Hock,B.D., Patton,W.N., Budhia,S., Mannari,D., Roberts,P. and McKenzie,J.L.

TITLE Human plasma contains a soluble form of CD86 which is present at elevated levels in some leukaemia patients

JOURNAL Leukemia 16 (5), 865-873 (2002)

PUBMED [11986949](#)

REMARK GeneRIF: a soluble form of CD86 encoded by an alternatively spliced transcript is present at elevated levels in blood in some leukaemia patients

REFERENCE 14 (bases 1 to 2781)

AUTHORS Suvas,S., Singh,V., Sahdev,S., Vohra,H. and Agrewala,J.N.

TITLE Distinct role of CD80 and CD86 in the regulation of the activation of B cell and B cell lymphoma

JOURNAL J. Biol. Chem. 277 (10), 7766-7775 (2002)

PUBMED [11726649](#)

REMARK GeneRIF: Thus, this study is the first demonstration of a distinct signaling event induced by CD80 and CD86 molecules in B cell lymphoma.

REFERENCE 15 (bases 1 to 2781)

AUTHORS Vasilevko,V., Ghochikyan,A., Holterman,M.J. and Agadjanyan,M.G.

TITLE CD80 (B7-1) and CD86 (B7-2) are functionally equivalent in the initiation and maintenance of CD4+ T-cell proliferation after activation with suboptimal doses of PHA

JOURNAL DNA Cell Biol. 21 (3), 137-149 (2002)

PUBMED [12015893](#)

REMARK GeneRIF: CD80 and CD86 molecules can substitute for each other in the initial activation of resting CD4(+) T cells and in the maintenance of their proliferative response

REFERENCE 16 (bases 1 to 2781)

AUTHORS Re,F., Arpinati,M., Testoni,N., Ricci,P., Terragna,C., Preda,P., Ruggeri,D., Senese,B., Chirumbolo,G., Martelli,V., Urbini,B., Baccarani,M., Tura,S. and Rondelli,D.

TITLE Expression of CD86 in acute myelogenous leukemia is a marker of dendritic/monocytic lineage

JOURNAL Exp. Hematol. 30 (2), 126-134 (2002)

PUBMED [11823047](#)

REMARK GeneRIF: In AML, CD86 is a marker of monocytic/dendritic lineage

REFERENCE 17 (bases 1 to 2781)  
AUTHORS Niemann-Masanek,U., Mueller,A., Yard,B.A., Waldherr,R. and van der Woude,F.J.  
TITLE B7-1 (CD80) and B7-2 (CD 86) expression in human tubular epithelial cells in vivo and in vitro  
JOURNAL Nephron 92 (3), 542-556 (2002)  
PUBMED [12372936](#)  
REMARK GeneRIF: After B7-1 and B7-2 induction, proximal tubular epithelial cells costimulate CD28 on T lymphocytes resulting in cytokine production.

REFERENCE 18 (bases 1 to 2781)  
AUTHORS Chang,T.T., Kuchroo,V.K. and Sharpe,A.H.  
TITLE Role of the B7-CD28/CTLA-4 pathway in autoimmune disease  
JOURNAL Curr. Dir. Autoimmun. 5, 113-130 (2002)  
PUBMED [11826754](#)  
REMARK GeneRIF: The B7-CD28/CTLA-4 costimulatory pathway has a dominant role in regulating T-cell activation. Antagonists enable graft survival and suppress autoimmunity.

REFERENCE 19 (bases 1 to 2781)  
AUTHORS Schwartz,J.C., Zhang,X., Fedorov,A.A., Nathenson,S.G. and Almo,S.C.  
TITLE Structural basis for co-stimulation by the human CTLA-4/B7-2 complex  
JOURNAL Nature 410 (6828), 604-608 (2001)  
PUBMED [11279501](#)  
REMARK GeneRIF: Structure in complex with CTLA-4; may represent a distinct signalling mechanism available to dimeric cell-surface receptors.

REFERENCE 20 (bases 1 to 2781)  
AUTHORS Bugeon,L. and Dallman,M.J.  
TITLE Costimulation of T cells  
JOURNAL Am. J. Respir. Crit. Care Med. 162 (4 Pt 2), S164-S168 (2000)  
PUBMED [11029388](#)

REFERENCE 21 (bases 1 to 2781)  
AUTHORS Jeannin,P., Magistrelli,G., Aubry,J.P., Caron,G., Gauchat,J.F., Renno,T., Herbault,N., Goetsch,L., Blaecke,A., Dietrich,P.Y., Bonnefoy,J.Y. and Delneste,Y.  
TITLE Soluble CD86 is a costimulatory molecule for human T lymphocytes  
JOURNAL Immunity 13 (3), 303-312 (2000)  
PUBMED [11021528](#)

REFERENCE 22 (bases 1 to 2781)  
AUTHORS Reeves,R.H., Patch,D., Sharpe,A.H., Borriello,F., Freeman,G.J., Edelhoff,S. and Disteche,C.  
TITLE The costimulatory genes Cd80 and Cd86 are linked on mouse chromosome 16 and human chromosome 3  
JOURNAL Mamm. Genome 8 (8), 581-582 (1997)  
PUBMED [9250865](#)

REFERENCE 23 (bases 1 to 2781)  
AUTHORS Jellis,C.L., Wang,S.S., Rennert,P., Borriello,F., Sharpe,A.H., Green,N.R. and Gray,G.S.  
TITLE Genomic organization of the gene coding for the costimulatory human B-lymphocyte antigen B7-2 (CD86)  
JOURNAL Immunogenetics 42 (2), 85-89 (1995)  
PUBMED [7541777](#)

REFERENCE 24 (bases 1 to 2781)  
AUTHORS Chen,C., Gault,A., Shen,L. and Nabavi,N.  
TITLE Molecular cloning and expression of early T cell costimulatory molecule-1 and its characterization as B7-2 molecule  
JOURNAL J. Immunol. 152 (10), 4929-4936 (1994)  
PUBMED [7513726](#)

REFERENCE 25 (bases 1 to 2781)  
AUTHORS Freeman,G.J., Gribben,J.G., Boussiotis,V.A., Ng,J.W., Restivo,V.A.

Jr., Lombard, L.A., Gray, G.S. and Nadler, L.M.  
 TITLE Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human  
 T cell proliferation  
 JOURNAL Science 262 (5135), 909-911 (1993)  
 PUBMED [7694363](#)  
 REFERENCE 26 (bases 1 to 2781)  
 AUTHORS Azuma, M., Ito, D., Yagita, H., Okumura, K., Phillips, J.H., Lanier, L.L.  
 and Somoza, C.  
 TITLE B70 antigen is a second ligand for CTLA-4 and CD28  
 JOURNAL Nature 366 (6450), 76-79 (1993)  
 PUBMED [7694153](#)  
 COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The  
 reference sequence was derived from [BC040261.1](#).  
 On Mar 18, 2003 this sequence version replaced [gi:28466994](#).

Summary: This gene encodes a type I membrane protein that is a member of the immunoglobulin superfamily. This protein is expressed by antigen-presenting cells, and it is the ligand for two proteins at the cell surface of T cells, CD28 antigen and cytotoxic T-lymphocyte-associated protein 4. Binding of this protein with CD28 antigen is a costimulatory signal for activation of the T-cell. Binding of this protein with cytotoxic T-lymphocyte-associated protein 4 negatively regulates T-cell activation and diminishes the immune response. Alternative splicing results in two transcript variants encoding different isoforms. Additional transcript variants have been described, but their full-length sequences have not been determined.

Transcript Variant: This variant (1) encodes the longer isoform (1) of this protein.

COMPLETENESS: complete on the 3' end.

FEATURES

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	go_component: plasma membrane [goid <a href="#">0005886</a> ] [evidence NR]
	[pmid 7513726];
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	go_process: positive regulation of cell proliferation [goid <a href="#">0008284</a> ] [evidence TAS] [pmid 7513726];
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## ORIGIN

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2701 attcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
2761 aaaaaaaaaa aaaaaaaaaa a
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//

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[NCBI](#) | [NLM](#) | [NIH](#)

Jun 8 2004 17:01:12



# results of BLAST

BLASTN 2.2.9 [May-01-2004]

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1089397542-7110-63957653711.BLASTQ4

**Query=**

(2781 letters)

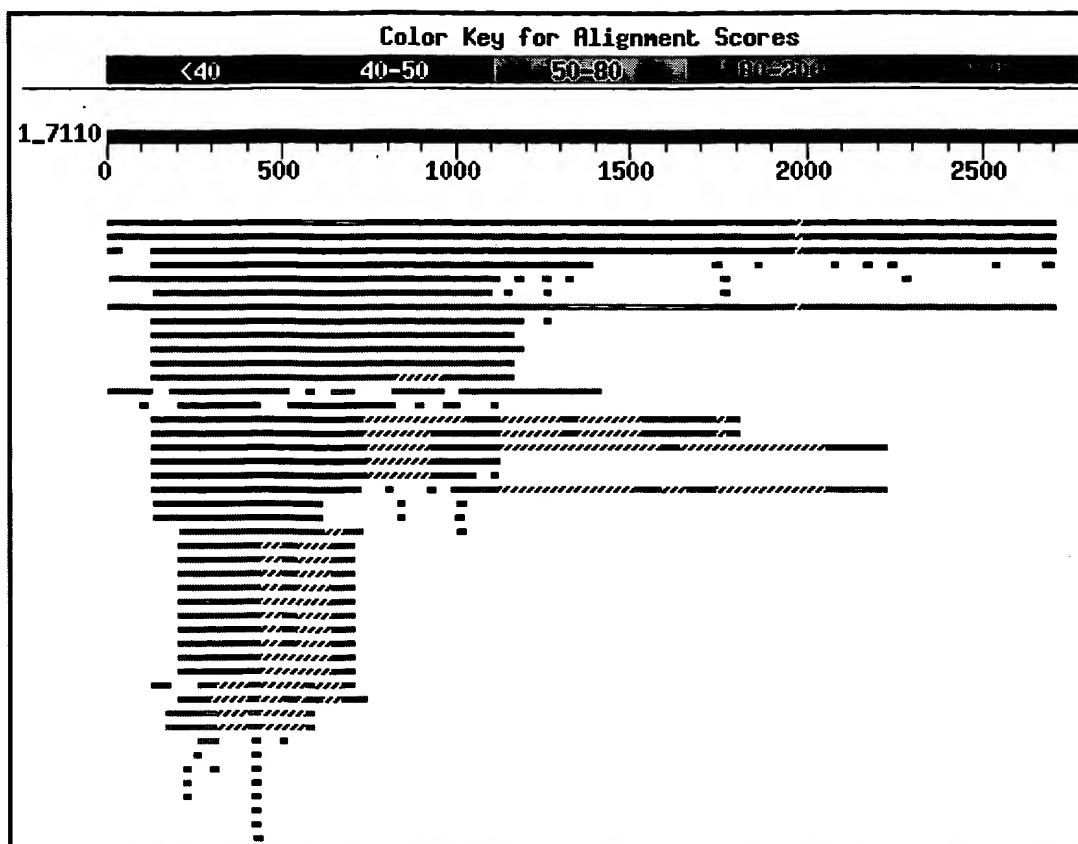
**Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)  
2,280,493 sequences; 11,051,402,435 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

## Distribution of 145 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments
--



Sequences producing significant alignments:				Score	E	
				(bits)	Value	
gi 29029571 ref NM_175862.2	Homo sapiens CD86 antigen (CD2...	3834	0.0			LU
gi 25955518 gb BC040261.1	Homo sapiens CD86 antigen (CD28 ...	3826	0.0			LU
gi 29029570 ref NM_006889.2	Homo sapiens CD86 antigen (CD2...	3578	0.0			LUG
gi 439838 gb U04343.1 HSU04343	Human CD86 antigen mRNA, com...	2504	0.0			LUG
gi 416368 gb L25259.1 HUMB72A	Human CTLA4 counter-receptor ...	2204	0.0			LUG
gi 49456642 emb CR541844.1	Homo sapiens full open reading ...	1921	0.0			
gi 16572839 gb AC068630.21	Homo sapiens 3 BAC RP11-289N10 ...	1798	0.0			
gi 13650019 gb AF344861.1 AF344861	Cercopithecus aethiops C...	1796	0.0			
gi 13650011 gb AF344857.1 AF344857	Macaca mulatta CD86 prot...	1784	0.0			
gi 13650000 gb AF344840.1 AF344840	Cercocebus torquatus aty...	1780	0.0			
gi 13655490 gb AF344851.1 AF344851	Macaca nemestrina CD86 p...	1721	0.0			
gi 13649983 gb AF344836.1 AF344836	Papio cynocephalus anubi...	1179	0.0			
gi 808032 gb U17722.1 HSB72S8	Human CTLA-4 counter-receptor...	805	0.0			L
gi 808028 gb U17718.1 HSB72S4	Human CTLA-4 counter-receptor...	660	0.0			
gi 808029 gb U17719.1 HSB72S5	Human CTLA-4 counter-receptor...	603	e-169			
gi 6572518 gb AF106827.1 AF106827	Canis familiaris truncate...	396	e-106			U
gi 6572516 gb AF106826.1 AF106826	Canis familiaris B7-2 pro...	396	e-106			LUG
gi 5381423 gb AF157827.1 AF157827	Felis catus CD86 antigen ...	361	5e-96			
gi 15418725 gb AY007704.1	Felis catus CD86 (CD86) mRNA, co...	361	5e-96			
gi 9796387 dbj AB030652.1	Felis catus mRNA for B-lymphocyt...	361	5e-96			
gi 755098 dbj D49842.1 RABCD86B	Oryctolagus cuniculus mRNA ...	355	3e-94			
gi 808030 gb U17720.1 HSB72S6	Human CTLA-4 counter-receptor...	293	1e-75			
gi 47523527 ref NM_214222.1	Sus scrofa CD86 protein (CD86)...	264	9e-67			LU



gi 2198558 gb L76099.1 PIGCD86G	Sus scrofa CD86 mRNA, compl...	264	9e-67	LU
gi 808025 gb U17715.1 HSB72S1	Human CTLA-4 counter-receptor...	258	6e-65	
gi 10803379 emb AJ291475.1 BTA291475	Bos taurus partial mRN...	153	2e-33	LU
gi 40217708 gb AC117662.13	Mus musculus chromosome 16, clo...	143	2e-30	
gi 4587845 gb AF065900.1 AF065900	Mus musculus strain SJL/J...	143	2e-30	LU
gi 4587843 gb AF065899.1 AF065899	Mus musculus strain B10.S...	143	2e-30	LUG
gi 4587841 gb AF065898.1 AF065898	Mus musculus strain C57BL...	143	2e-30	LU
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gi 26348035 dbj AK079513.1	Mus musculus 16 days neonate th...	143	2e-30	LU
gi 432478 gb L25606.1 MUSB72X	Murine B7-2 mRNA, complete cds	143	2e-30	LUG
gi 546694 gb S70108.1 S70108	early T cell costimulatory mol...	143	2e-30	L
gi 15489434 gb BC013807.1	Mus musculus CD86 antigen, mRNA ...	141	9e-30	LUG
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gi 808027 gb U17717.1 HSB72S3	Human CTLA-4 counter-receptor...	105	5e-19	
gi 25188157 dbj AB085744.1	Mesocricetus auratus mRNA for B...	101	8e-18	
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gi 3851167 gb AF099105.1 AF099105	Homo sapiens B7.2 antigen...	85	5e-13	
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gi 11464988 ref NM_020081.1	Rattus norvegicus CD86 antigen...	73	2e-09	LUG
gi 2627024 dbj D50558.1	Rattus norvegicus mRNA for membran...	73	2e-09	LUG
gi 940936 gb U31330.1 RNU31330	Rattus norvegicus B7-2 mRNA,...	63	2e-06	LU
gi 1127751 gb U39463.1 MMB72G08	Mus musculus B7-2 gene, exon 8	57	1e-04	L
gi 21217730 gb AY095931.1	Meriones unguiculatus costimulat...	50	0.026	
gi 2338551 gb AF013277.1 AF013277	Bombyx mori topoisomerase...	50	0.026	U
gi 26801335 gb AC121585.3	Mus musculus BAC clone RP23-265M...	46	0.41	
gi 3790157 emb AL022146.1 HS780M13	Human DNA sequence from ...	46	0.41	G
gi 16603965 gb AC076968.38	Homo sapiens 12 BAC RP11-686F15...	44	1.6	
gi 21591818 gb AC109992.6	Homo sapiens 3 BAC RP11-383G6 (R...	44	1.6	
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gi 47900647 gb AC149300.1	Populus balsamifera subsp. trich...	44	1.6	
gi 28445790 emb AL928981.7	Mouse DNA sequence from clone R...	44	1.6	
gi 38259256 gb AC125324.4	Mus musculus BAC clone RP23-284J...	44	1.6	
gi 31376490 gb AC122483.5	Mus musculus BAC clone RP24-366B...	42	6.3	
gi 23499649 gb AC117238.3	Mus musculus BAC clone RP24-82N1...	42	6.3	
gi 22138622 gb AC121875.2	Mus musculus BAC clone RP24-1250...	42	6.3	
gi 34447295 gb AC110918.9	Mus musculus chromosome 5, clone...	42	6.3	
gi 36435777 gb AC110557.10	Mus musculus chromosome 5, clon...	42	6.3	
gi 40225660 gb BC032109.2	Homo sapiens suppression of tumo...	42	6.3	LU
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gi 29150346 gb AC136940.2	Homo sapiens chromosome 5 clone ...	42	6.3	
gi 29569250 gb AC106795.3	Homo sapiens chromosome 5 clone ...	42	6.3	
gi 22450644 gb AC018628.13	Homo sapiens chromosome 17, clo...	42	6.3	
gi 46358393 gb AC125151.4	Mus musculus BAC clone RP24-355K...	42	6.3	
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gi 46879216 gb AC126006.21	Medicago truncatula clone mth2-...	42	6.3	
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gi 33186784 emb AL772310.27	Mouse DNA sequence from clone ...	42	6.3	
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gi 23093569 emb AL772344.4	Mouse DNA sequence from clone R...	42	6.3	
gi 24414658 emb AL663067.14	Mouse DNA sequence from clone ...	42	6.3	
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gi 13365868 dbj AB056772.1	Macaca fascicularis brain cDNA ...	42	6.3	G
gi 18479121 dbj AP004582.2	Homo sapiens genomic DNA, chrom...	42	6.3	
gi 21541280 emb AL096864.12	HSJ993D20 Human DNA sequence fr...	42	6.3	
gi 21264628 ref NM_013437.2	Homo sapiens suppression of tu...	42	6.3	LU G

## Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|29029571|ref|NM\_175862.2| LU Homo sapiens CD86 antigen (CD28 antigen ligand (CD86), transcript variant 1, mRNA  
Length = 2781

Score = 3834 bits (1934), Expect = 0.0

Identities = 1952/1961 (99%)

Strand = Plus / Plus

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Strand = Plus / Plus

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Query: 2471 ggatggggcagtcctctgcccaaacataaagagaactctggggagcctgagccacaaaaat 2530

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Sbjct: 2471 ggatggggcagtcctctgcccaaacataaagagaactctggggagcctgagccacaaaaat 2530

Query: 2531 gttcctttattttatgtaaaccctcaagggttatagactgcatgctagacaagcttgtc 2590

|||||  
Sbjct: 2531 gttcctttattttatgtaaaccctcaagggttatagactgcatgctagacaagcttgtc 2590

Query: 2591 catgtaatatcccatgtttttaccctgccctgccttgattagactcctagcacctggc 2650

|||||  
Sbjct: 2591 catgtaatatcccatgtttttaccctgccctgccttgattagactcctagcacctggc 2650

Query: 2651 tagtttctaacatgttttgtgcagcacagtttttaataaatgcttgttacattc 2704

|||||  
Sbjct: 2651 tagtttctaacatgttttgtgcagcacagtttttaataaatgcttgttacattc 2704

☐ >gi|25955518|gb|BC040261.1| **LU** Homo sapiens CD86 antigen (CD28 antigen ligand ;  
transcript variant 1, mRNA (cDNA clone MGC:34413  
IMAGE:5173789), complete cds  
Length = 2781

Score = 3826 bits (1930), Expect = 0.0

Identities = 1951/1961 (99%)

Strand = Plus / Plus

Query: 1 ggaaggcttgacaggggtgaaagctttgcttctctgctgctgtaacagggactagcacag 60

|||||  
Sbjct: 1 ggaaggcttgacaggggtgaaagctttgcttctctgctgctgtaacagggactagcacag 60

Query: 61 acacacggatgagtgggggtcatttccagatattaggtcacagcagaagcagccaaaatgg 120

|||||  
Sbjct: 61 acacacggatgagtgggggtcatttccagatattaggtcacagcagaagcagccaaaatgg 120

Query: 121 atccccagtgactatgggactgagtaacattctctttgtgatggccttctgctctctg 180

|||||  
Sbjct: 121 atccccagtgactatgggactgagtaacattctctttgtgatggccttctgctctctg 180

Query: 181 gtgctgctcctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaat 240

|||||  
Sbjct: 181 gtgctgctcctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaat 240

Query: 241 ttgcaaactctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaa 300

|||||  
Sbjct: 241 ttgcaaactctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaa 300

Query: 301 acttggttctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagt 360

Sbjct: 301 |||  
acttggttctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagt 360

Query: 361 atatgggccgcacaagttttgattcggacagttggaccctgagacttcacaatcttcaga 420  
|||  
Sbjct: 361 atatgggccgcacaagttttgattcggacagttggaccctgagacttcacaatcttcaga 420

Query: 421 tcaaggacaagggcttgtatcaatgtatcatccatcacaaaagcccacaggaatgattc 480  
|||  
Sbjct: 421 tcaaggacaagggcttgtatcaatgtatcatccatcacaaaagcccacaggaatgattc 480

Query: 481 gcatccaccagatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatag 540  
|||  
Sbjct: 481 gcatccaccagatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatag 540

Query: 541 taccaatttctaataataacagaaaatgtgtacataaatttgacctgctcatctatacacg 600  
|||  
Sbjct: 541 taccaatttctaataataacagaaaatgtgtacataaatttgacctgctcatctatacacg 600

Query: 601 gttaccagaacctaagaagatgagtgtttgcgaagaaccaagaattcaactatcgagt 660  
|||  
Sbjct: 601 gttaccagaacctaagaagatgagtgtttgcgaagaaccaagaattcaactatcgagt 660

Query: 661 atgatggtattatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatca 720  
|||  
Sbjct: 661 atgatggtattatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatca 720

Query: 721 gcttgtctgtttcattccctgatgttacgagcaatatgacctcttctgtattctggaaa 780  
|||  
Sbjct: 721 gcttgtctgtttcattccctgatgttacgagcaatatgacctcttctgtattctggaaa 780

Query: 781 ctgacaagacgcggcttttatcttcaccttctctatagagcttgaggaccctcagcctc 840  
|||  
Sbjct: 781 ctgacaagacgcggcttttatcttcaccttctctatagagcttgaggaccctcagcctc 840

Query: 841 cccagaccacattccttgattacagctgtacttccaacagttattatatgtgtgatgg 900  
|||  
Sbjct: 841 cccagaccacattccttgattacagctgtacttccaacagttattatatgtgtgatgg 900

Query: 901 ttttctgtctaattctatggaaatggaagaagaagaagcggcctcgcaactcttataaat 960  
|||  
Sbjct: 901 ttttctgtctaattctatggaaatggaagaagaagaagcggcctcgcaactcttataaat 960

Query: 961 gtggaaccaacacaatggagaggggaagagagtgaacagaccaagaaaagagaaaaatcc 1020  
|||  
Sbjct: 961 gtggaaccaacacaatggagaggggaagagagtgaacagaccaagaaaagagaaaaatcc 1020

Query: 1021 atatacctgaaagatctgatgaagcccagcgtgtttttaaaagtgcgaagacatcttcat 1080

|||||  
Sbjct: 1021 atatacctgaaagatctgatgaaacccagcgtgtttttaaaagtctgaagacatcttcat 1080

Query: 1081 gcgacaaaagtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttt 1140  
|||||  
Sbjct: 1081 gcgacaaaagtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttt 1140

Query: 1141 tctaccctttcctttgtaagttcctgggcaacctttttgatttcttccagaaggcaaaaa 1200  
|||||  
Sbjct: 1141 tctaccctttcctttgtaagttcctgggcaacctttttgatttcttccagaaggcaaaaa 1200

Query: 1201 gacattaccatgagtaataagggggctccaggactccctctaagtggaatagcctccctg 1260  
|||||  
Sbjct: 1201 gacattaccatgagtaataagggggctccaggactccctctaagtggaatagcctccctg 1260

Query: 1261 taactccagctctgctccgtatgccaaaggagactttaattctcttactgcttcttttc 1320  
|||||  
Sbjct: 1261 taactccagctctgctccgtatgccaaaggagactttaattctcttactgcttcttttc 1320

Query: 1321 acttcagagcacacttatgggccaagcccagcttaatggctcatgacctggaaataaaat 1380  
|||||  
Sbjct: 1321 acttcagagcacacttatgggccaagcccagcttaatggctcatgacctggaaataaaat 1380

Query: 1381 ttaggaccaatacctcctccagatcagattcttctcttaatttcatagattgtgnnnnnn 1440  
|||||  
Sbjct: 1381 ttaggaccaatacctcctccagatcagattcttctcttaatttcatagattgtgtttttt 1440

Query: 1441 nnnaaatagacctctcaatttctggaaaactgccttttatctgccagaattctaagctg 1500  
|||||  
Sbjct: 1441 tttaaatagacctctcaatttctggaaaactgccttttatctgccagaattctaagctg 1500

Query: 1501 gtgccccactgaatcttgtgtacctgtgactaaacaactacctcctcagctctgggtggga 1560  
|||||  
Sbjct: 1501 gtgccccactgaatcttgtgtacctgtgactaaacaactacctcctcagctctgggtggga 1560

Query: 1561 cttatgtatttatgaccttatagtgttaatatcttgaaacatagagatctatgtactgta 1620  
|||||  
Sbjct: 1561 cttatgtatttatgaccttatagtgttaatatcttgaaacatagagatctatgtactgta 1620

Query: 1621 atagtgtgattactatgctctagagaaaagtctaccctgctaaggagttctcatccctc 1680  
|||||  
Sbjct: 1621 atagtgtgattactatgctctagagaaaagtctaccctgctaaggagttctcatccctc 1680

Query: 1681 tgtcagggtcagtaaggaaaacgggtggcctagggtacaggcaacaatgagcagaccaacc 1740  
|||||  
Sbjct: 1681 tgtcagggtcagtaaggaaaacgggtggcctagggtacaggcaacaatgagcagaccaacc 1740

Query: 1741 taaatttggggaaattaggagaggcagagatagaacctggagccacttctatctgggctg 1800



Score = 1415 bits (714), Expect = 0.0  
Identities = 714/714 (100%)  
Strand = Plus / Plus

7/9/2004


Query: 2411 gagacagatatactgggagaaaatgactttgaaaaacctggctctaaggtgggatcactaag 2470  
|||||  
Sbjct: 2411 gagacagatatactgggagaaaatgactttgaaaaacctggctctaaggtgggatcactaag 2470

Query: 2471 ggatggggcagtctctgcccacataaagagaactctggggagcctgagccacaaaaat 2530  
|||||  
Sbjct: 2471 ggatggggcagtctctgcccacataaagagaactctggggagcctgagccacaaaaat 2530

Query: 2531 gttcctttattttatgtaaaccctcaagggttatagactgccatgctagacaagcttgct 2590  
|||||  
Sbjct: 2531 gttcctttattttatgtaaaccctcaagggttatagactgccatgctagacaagcttgct 2590

Query: 2591 catgtaatattcccatgtttttaccctgcccctgccttgattagactcctagcacctggc 2650  
|||||  
Sbjct: 2591 catgtaatattcccatgtttttaccctgcccctgccttgattagactcctagcacctggc 2650

Query: 2651 tagtttctaacatgttttgtgcagcacagtttttaataaatgcttggttacattc 2704  
|||||  
Sbjct: 2651 tagtttctaacatgttttgtgcagcacagtttttaataaatgcttggttacattc 2704

 >gi|29029570|ref|NM\_006889.2| **LUIG** Homo sapiens CD86 antigen (CD28 antigen ligand) (CD86), transcript variant 2, mRNA  
Length = 2794

Score = 3578 bits (1805), Expect = 0.0  
Identities = 1823/1832 (99%)  
Strand = Plus / Plus

Query: 130 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc 189  
|||||  
Sbjct: 143 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc 202

Query: 190 ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact 249  
|||||  
Sbjct: 203 ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact 262

Query: 250 ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc 309  
|||||  
Sbjct: 263 ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc 322

Query: 310 tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcc 369  
|||||  
Sbjct: 323 tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcc 382

Query: 370 gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca 429  
|||||  
Sbjct: 383 gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca 442

Query: 430 agggcttgatatcaatgtatcatccatcacaaaaagccacaggaatgattcgcatccacc 489  
|||||  
Sbjct: 443 agggcttgatatcaatgtatcatccatcacaaaaagccacaggaatgattcgcatccacc 502

Query: 490 agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaattt 549  
|||||  
Sbjct: 503 agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaattt 562

Query: 550 ctaatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttaccag 609  
|||||  
Sbjct: 563 ctaatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttaccag 622

Query: 610 aacctaagaagatgagtggttttgctaagaaccaagaattcaactatcgagtatgatggta 669  
|||||  
Sbjct: 623 aacctaagaagatgagtggttttgctaagaaccaagaattcaactatcgagtatgatggta 682

Query: 670 ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgctg 729  
|||||  
Sbjct: 683 ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgctg 742

Query: 730 tttcatccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaaga 789  
|||||  
Sbjct: 743 tttcatccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaaga 802

Query: 790 cgcggtttttatcttcacctttctctatagagcttgaggacctcagcctccccagacc 849  
|||||  
Sbjct: 803 cgcggtttttatcttcacctttctctatagagcttgaggacctcagcctccccagacc 862

Query: 850 acattccttggtattacagctgtacttccaacagttattatatgtgtgatgggttttctgtc 909  
|||||  
Sbjct: 863 acattccttggtattacagctgtacttccaacagttattatatgtgtgatgggttttctgtc 922

Query: 910 taattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaacca 969  
|||||  
Sbjct: 923 taattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaacca 982

Query: 970 acacaatggagaggggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctg 1029  
|||||  
Sbjct: 983 acacaatggagaggggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctg 1042

Query: 1030 aaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaa 1089  
|||||  
Sbjct: 1043 aaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaa 1102

Query: 1090 gtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttttctaccctt 1149  
|||||  
Sbjct: 1103 gtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttttctaccctt 1162

Query: 1150 tcctttgtaagttcctgggcaacctttttgatttcttccagaaggcaaaaagacattacc 1209  
|||||  
Sbjct: 1163 tcctttgtaagttcctgggcaacctttttgatttcttccagaaggcaaaaagacattacc 1222

Query: 1210 atgagtaataagggggctccaggactccctctaagtggaatagcctccctgtaactccag 1269  
|||||  
Sbjct: 1223 atgagtaataagggggctccaggactccctctaagtggaatagcctccctgtaactccag 1282

Query: 1270 ctctgctccgtatgccaagaggagactttaattctcttactgcttcttttcacttcagag 1329  
|||||  
Sbjct: 1283 ctctgctccgtatgccaagaggagactttaattctcttactgcttcttttcacttcagag 1342

Query: 1330 cacacttatgggccaagcccagcttaatggctcatgacctggaaataaaaatttaggacca 1389  
|||||  
Sbjct: 1343 cacacttatgggccaagcccagcttaatggctcatgacctggaaataaaaatttaggacca 1402

Query: 1390 atacctcctccagatcagattcttctcttaatttcatagattgtgnnnnnnnnnaaatag 1449  
|||||  
Sbjct: 1403 atacctcctccagatcagattcttctcttaatttcatagattgtgttttttttaaatag 1462

Query: 1450 acctctcaatttctggaaaactgccttttatctgccagaattctaagctggtgccccac 1509  
|||||  
Sbjct: 1463 acctctcaatttctggaaaactgccttttatctgccagaattctaagctggtgccccac 1522

Query: 1510 tgaatcttgtgtacctgtgactaaacaactacctcctcagtctgggtgggacttatgtat 1569  
|||||  
Sbjct: 1523 tgaatcttgtgtacctgtgactaaacaactacctcctcagtctgggtgggacttatgtat 1582

Query: 1570 ttatgaccttatagtgttaatatcttgaaacatagagatctatgtactgtaatagtgtga 1629  
|||||  
Sbjct: 1583 ttatgaccttatagtgttaatatcttgaaacatagagatctatgtactgtaatagtgtga 1642

Query: 1630 ttactatgctctagagaaaagtctacccctgctaaggagttctcatccctctgtcaggg 1689  
|||||  
Sbjct: 1643 ttactatgctctagagaaaagtctacccctgctaaggagttctcatccctctgtcaggg 1702

Query: 1690 cagtaaggaaaacggtggcctagggtagaggcaacaatgagcagaccaacctaatttgg 1749  
|||||  
Sbjct: 1703 cagtaaggaaaacggtggcctagggtagaggcaacaatgagcagaccaacctaatttgg 1762

Query: 1750 ggaaattaggagaggcagagatagaacctggagccacttctatctgggctgttgctaata 1809  
|||||  
Sbjct: 1763 ggaaattaggagaggcagagatagaacctggagccacttctatctgggctgttgctaata 1822

Query: 1810 ttgaggaggcttgccccacccaacaagccatagtggagagaactgaataaacaggaaaat 1869  
|||||  
Sbjct: 1823 ttgaggaggcttgccccacccaacaagccatagtggagagaactgaataaacaggaaaat 1882

Query: 1870 gccagagcttgtgaaccctgtttctcttgaagaactgactagtgagatggcctggggaag 1929  
|||||  
Sbjct: 1883 gccagagcttgtgaaccctgtttctcttgaagaactgactagtgagatggcctggggaag 1942

Query: 1930 ctgtgaaagaaccaaagagatcacaatactc 1961  
|||||  
Sbjct: 1943 ctgtgaaagaaccaaagagatcacaatactc 1974

Score = 1415 bits (714), Expect = 0.0  
Identities = 714/714 (100%)  
Strand = Plus / Plus

Query: 1991 tcttgatccacagaaatacatgaaatgtctggtctgtccaccccatcaacaagtcttgaa 2050  
|||||  
Sbjct: 2004 tcttgatccacagaaatacatgaaatgtctggtctgtccaccccatcaacaagtcttgaa 2063

Query: 2051 acaagcaacagatggatagtctgtccaaatggacataagacagacagcagtttccctggt 2110  
|||||  
Sbjct: 2064 acaagcaacagatggatagtctgtccaaatggacataagacagacagcagtttccctggt 2123

Query: 2111 ggtcagggaggggttttggtgatacccaagttattgggatgtcatcttcctggaagcaga 2170  
|||||  
Sbjct: 2124 ggtcagggaggggttttggtgatacccaagttattgggatgtcatcttcctggaagcaga 2183

Query: 2171 gctggggagggagagccatcaccttgataatgggatgaatggaaggaggcttaggacttt 2230  
|||||  
Sbjct: 2184 gctggggagggagagccatcaccttgataatgggatgaatggaaggaggcttaggacttt 2243

Query: 2231 ccactcctggctgagagaggaagagctgcaacggaattaggaagaccaagacacagatca 2290  
|||||  
Sbjct: 2244 ccactcctggctgagagaggaagagctgcaacggaattaggaagaccaagacacagatca 2303

Query: 2291 cccggggcttacttagcctacagatgtcctacgggaacgtgggctggcccagcatagggc 2350  
|||||  
Sbjct: 2304 cccggggcttacttagcctacagatgtcctacgggaacgtgggctggcccagcatagggc 2363

Query: 2351 tagcaaatttgagttggatgattgttttctcaaggcaaccagaggaaacttgcataca 2410  
|||||  
Sbjct: 2364 tagcaaatttgagttggatgattgttttctcaaggcaaccagaggaaacttgcataca 2423

Query: 2411 gagacagatatactgggagaaatgactttgaaaacctggctctaaggtgggatcactaag 2470  
|||||  
Sbjct: 2424 gagacagatatactgggagaaatgactttgaaaacctggctctaaggtgggatcactaag 2483

Query: 2471 ggatggggcagtcctctgcccaaacataaagagaactctggggagcctgagccacaaaaat 2530  
|||||  
Sbjct: 2484 ggatggggcagtcctctgcccaaacataaagagaactctggggagcctgagccacaaaaat 2543

Query: 2531 gttccctttattttatgtaaaccctcaagggttatagactgccatgctagacaagcttgct 2590  
|||||  
Sbjct: 2544 gttccctttattttatgtaaaccctcaagggttatagactgccatgctagacaagcttgct 2603

Query: 2591 catgtaatattcccatgtttttaccctgcccctgccttgattagactcctagcacctggc 2650  
|||||  
Sbjct: 2604 catgtaatattcccatgtttttaccctgcccctgccttgattagactcctagcacctggc 2663

Query: 2651 tagtttctaacatgttttgtgcagcacagttttaataaatgcttgttacattc 2704  
|||||  
Sbjct: 2664 tagtttctaacatgttttgtgcagcacagttttaataaatgcttgttacattc 2717

☐ >gi|439838|gb|U04343.1|HSU04343 **LUG** Human CD86 antigen mRNA, complete cds  
Length = 1424

Score = 2504 bits (1263), Expect = 0.0  
Identities = 1263/1263 (100%)  
Strand = Plus / Plus

Query: 130 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc 189  
|||||  
Sbjct: 143 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc 202

Query: 190 ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact 249  
|||||  
Sbjct: 203 ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact 262

Query: 250 ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc 309  
|||||  
Sbjct: 263 ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc 322

Query: 310 tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcc 369  
|||||  
Sbjct: 323 tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcc 382

Query: 370 gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca 429  
|||||  
Sbjct: 383 gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca 442

Query: 430 agggcttgatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacc 489  
|||||  
Sbjct: 443 agggcttgatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacc 502

Query: 490 agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtagcaattt 549  
|||||  
Sbjct: 503 agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtagcaattt 562

Query: 550 ctaatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttaccag 609  
|||||  
Sbjct: 563 ctaatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttaccag 622

Query: 610 aacctaagaagatgagtgttttgctaagaaccaagaattcaactatcgagtatgatggta 669  
|||||  
Sbjct: 623 aacctaagaagatgagtgttttgctaagaaccaagaattcaactatcgagtatgatggta 682

Query: 670 ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctg 729  
|||||  
Sbjct: 683 ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctg 742

Query: 730 ttccattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaaga 789  
|||||  
Sbjct: 743 ttccattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaaga 802

Query: 790 cgcggtttttatcttcacctttctctatagagcttgaggacctcagcctccccagacc 849  
|||||  
Sbjct: 803 cgcggtttttatcttcacctttctctatagagcttgaggacctcagcctccccagacc 862

Query: 850 acattccttggtattacagctgtacttccaacagttattatatgtgtgatggttttctgtc 909  
|||||  
Sbjct: 863 acattccttggtattacagctgtacttccaacagttattatatgtgtgatggttttctgtc 922

Query: 910 taattctatggaaatggaagaagaagaagcggtctcgcaactcttataaatgtggaacca 969  
|||||  
Sbjct: 923 taattctatggaaatggaagaagaagaagcggtctcgcaactcttataaatgtggaacca 982

Query: 970 acacaatggagaggggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctg 1029  
|||||  
Sbjct: 983 acacaatggagaggggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctg 1042

Query: 1030 aaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaa 1089  
|||||  
Sbjct: 1043 aaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaa 1102

Query: 1090 gtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttttctaccctt 1149  
|||||  
Sbjct: 1103 gtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttttctaccctt 1162

Query: 1150 tcctttgtaagttcctgggcaacctttttgatttcttccagaaggcaaaaagacattacc 1209  
|||||  
Sbjct: 1163 tcctttgtaagttcctgggcaacctttttgatttcttccagaaggcaaaaagacattacc 1222

Query: 1210 atgagtaataaggggggtccaggactccctctaagtggaatagcctccctgtaactccag 1269  
|||||  
Sbjct: 1223 atgagtaataaggggggtccaggactccctctaagtggaatagcctccctgtaactccag 1282

Query: 1270 ctctgctccgtatgccaagaggagactttaattctcttactgcttcttttcacttcagag 1329  
 |||  
 Sbjct: 1283 ctctgctccgtatgccaagaggagactttaattctcttactgcttcttttcacttcagag 1342

Query: 1330 cacacttatgggccaagcccagcttaatgggtcatgacctggaaataaaatttaggacca 1389  
 |||  
 Sbjct: 1343 cacacttatgggccaagcccagcttaatgggtcatgacctggaaataaaatttaggacca 1402

Query: 1390 ata 1392  
 |||  
 Sbjct: 1403 ata 1405

☐ >gi|416368|gb|L25259.1|HUMB72A **LUG** Human CTLA4 counter-receptor (B7-2) mRNA, c  
 Length = 1112

Score = 2204 bits (1112), Expect = 0.0  
 Identities = 1112/1112 (100%)  
 Strand = Plus / Plus

Query: 11 cacagggtgaaagctttgcttctctgctgctgtaacagggactagcacagacacacggat 70  
 |||  
 Sbjct: 1 cacagggtgaaagctttgcttctctgctgctgtaacagggactagcacagacacacggat 60

Query: 71 gagtgggggtcatttcagatattaggtcacagcagaagcagccaaatggatccccagtg 130  
 |||  
 Sbjct: 61 gagtgggggtcatttcagatattaggtcacagcagaagcagccaaatggatccccagtg 120

Query: 131 cactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctcc 190  
 |||  
 Sbjct: 121 cactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctcc 180

Query: 191 tctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatgtgcaaactc 250  
 |||  
 Sbjct: 181 tctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatgtgcaaactc 240

Query: 251 tcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttct 310  
 |||  
 Sbjct: 241 tcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttct 300

Query: 311 gaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccg 370  
 |||  
 Sbjct: 301 gaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccg 360

Query: 371 cacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggacaa 430  
 |||  
 Sbjct: 361 cacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggacaa 420

Query: 431 gggcttgatatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacca 490



```

Sbjct: 421  |||||
gggcttgatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacca 480

Query: 491  gatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaatttc 550
          |||||
Sbjct: 481  gatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaatttc 540

Query: 551  taatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttaccaga 610
          |||||
Sbjct: 541  taatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttaccaga 600

Query: 611  acctaagaagatgagtggttttgctaagaaccaagaattcaactatcgagtatgatggat 670
          |||||
Sbjct: 601  acctaagaagatgagtggttttgctaagaaccaagaattcaactatcgagtatgatggat 660

Query: 671  tatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgctgt 730
          |||||
Sbjct: 661  tatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgctgt 720

Query: 731  ttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaagac 790
          |||||
Sbjct: 721  ttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaagac 780

Query: 791  gcggcttttatcttcacctttctctatagagcttgaggaccctcagcctccccagacca 850
          |||||
Sbjct: 781  gcggcttttatcttcacctttctctatagagcttgaggaccctcagcctccccagacca 840

Query: 851  cattccttgattacagctgtacttccaacagttattatatgtgtgatggttttctgtct 910
          |||||
Sbjct: 841  cattccttgattacagctgtacttccaacagttattatatgtgtgatggttttctgtct 900

Query: 911  aattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaaccaa 970
          |||||
Sbjct: 901  aattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaaccaa 960

Query: 971  cacaatggagaggggaagagagtgaacagaccaagaaaagagaaaaatccatatacctga 1030
          |||||
Sbjct: 961  cacaatggagaggggaagagagtgaacagaccaagaaaagagaaaaatccatatacctga 1020

Query: 1031 aagatctgatgaagcccagcgtgttttttaaagttcgaagacatcttcatgcgacaaaag 1090
          |||||
Sbjct: 1021 aagatctgatgaagcccagcgtgttttttaaagttcgaagacatcttcatgcgacaaaag 1080

Query: 1091 tgatacatgtttttaattaaagagtaaagccc 1122
          |||||
Sbjct: 1081 tgatacatgtttttaattaaagagtaaagccc 1112
```

Score = 1921 bits (969), Expect = 0.0  
Identities = 969/969 (100%)  
Strand = Plus / Plus

Query: 675 cagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctgtttca 734  
 |||  
 Sbjct: 541 cagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctgtttca 600

Query: 735 ttccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaagacgcgg 794  
 |||  
 Sbjct: 601 ttccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaagacgcgg 660

Query: 795 cttttatcttcacctttctctatagagcttgaggaccctcagcctccccagaccacatt 854  
 |||  
 Sbjct: 661 cttttatcttcacctttctctatagagcttgaggaccctcagcctccccagaccacatt 720

Query: 855 ccttggttacagctgtacttccaacagttattatatgtgtgatgggtttctgtctaatt 914  
 |||  
 Sbjct: 721 ccttggttacagctgtacttccaacagttattatatgtgtgatgggtttctgtctaatt 780

Query: 915 ctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaaccaacaca 974  
 |||  
 Sbjct: 781 ctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaaccaacaca 840

Query: 975 atggagaggggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctgaaaga 1034  
 |||  
 Sbjct: 841 atggagaggggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctgaaaga 900

Query: 1035 tctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaagtgat 1094  
 |||  
 Sbjct: 901 tctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaagtgat 960

Query: 1095 acatgtttt 1103  
 |||  
 Sbjct: 961 acatgtttt 969

☐ >gi|16572839|gb|AC068630.21| ☒ Homo sapiens 3 BAC RP11-289N10 (Roswell Park Canc  
 Library) complete sequence  
 Length = 164161

Score = 1798 bits (907), Expect = 0.0  
 Identities = 944/957 (98%), Gaps = 3/957 (0%)  
 Strand = Plus / Minus

Query: 1008 agagaaaaaatccatatacctgaaagatctgatgaagcccagcgtgtttttaaaagttcg 1067  
 |||  
 Sbjct: 86502 agagaaaaaatccatatacctgaaagatctgatgaagcccagcgtgtttttaaaagttcg 86443

Query: 1068 aagacatcttcatgcgacaaaagtgatacatgtttttaattaaagagtaaagcccataca 1127  
 |||  
 Sbjct: 86442 aagacatcttcatgcgacaaaagtgatacatgtttttaattaaagagtaaagcccataca 86383

Query: 1128 agtattcattttttctaccctttcctttgtaagttcctgggcaacctttttgatttcttc 1187  
 |||  
 Sbjct: 86382 agtattcattttttctaccctttcctttgtaagttcctgggcaacctttttgatttcttc 86323

Query: 1188 cagaaggcaaaaagacattaccatgagtaataagggggctccaggactccctctaagtgg 1247  
|||||  
Sbjct: 86322 cagaaggcaaaaagacattaccatgagtaataagggggctccaggactccctctaagtgg 86263

Query: 1248 aatagcctccctgtaactccagctctgctccgtagccaagaggagactttaattctctt 1307  
|||||  
Sbjct: 86262 aatagcctccctgtaactccagctctgctccgtagccaagaggagactttaattctctt 86203

Query: 1308 actgcttcttttcacttcagagcacacttatgggccaagcccagcttaatggctcatgac 1367  
|||||  
Sbjct: 86202 actgcttcttttcacttcagagcacacttatgggccaagcccagcttaatggctcatgac 86143

Query: 1368 ctggaaataaaaatttaggaccaatacctcctccagatcagattcttctcttaatttcata 1427  
|||||  
Sbjct: 86142 ctggaaataaaaatttaggaccaatacctcctccagatcagattcttctcttaatttcata 86083

Query: 1428 gattgtgnnnnnnnn-aaatagacctctcaatttctggaaaactgccttttatctgccc 1486  
|||||  
Sbjct: 86082 gattgtgttttttttttaaatagacctctcaatttctggaaaactgccttttatctgccc 86023

Query: 1487 agaattctaagctgggtgccccactgaatcttgtgt--acctgtgactaaacaactacctc 1544  
|||||  
Sbjct: 86022 agaattctaagctgggtgccccactgaatttgtgtgtacctgtgactaaacaactacctc 85963

Query: 1545 ctgagtctgggtgggacttatgtatttatgaccttatagtgttaatatcttgaaacatag 1604  
|||||  
Sbjct: 85962 ctgagtctgggtgggacttatgtatttatgaccttatagtgttaatatcttgaaacatag 85903

Query: 1605 agatctatgtactgtaatagtgtgattactatgctctagagaaaagtctaccctgctaa 1664  
|||||  
Sbjct: 85902 agatctatgtactgtaatagtgtgattactatgctctagagaaaagtctaccctgctaa 85843

Query: 1665 ggagttctcatccctctgtcaggggtcagtaaggaaaacgggtggcctaggggtacaggcaac 1724  
|||||  
Sbjct: 85842 ggagttctcatccctctgtcaggggtcagtaaggaaaacgggtggcctaggggtacaggcaac 85783

Query: 1725 aatgagcagaccaacctaatttggggaaattaggagaggcagagatagaacctggagcc 1784  
|||||  
Sbjct: 85782 aatgagcagaccaacctaatttggggaaattaggagaggcagagatagaacctggagcc 85723

Query: 1785 acttctatctgggctgttgctaatttgaggaggcttgccccaccaacaagccatagtgt 1844  
|||||  
Sbjct: 85722 acttctatctgggctgttgctaatttgaggaggcttgccccaccaacaagccatagtgt 85663

Query: 1845 gagagaactgaataaacaggaaaatgccagagcttgtgaaccctgtttctcttgagaac 1904  
|||||  
Sbjct: 85662 gagagaactgaataaacaggaaaatgccagagcttgtgaaccctgtttctcttgagaac 85603

Query: 1905 tgactagtgagatggcctggggaagctgtgaaagaacccaaaagagatcacatactc 1961  
|||||  
Sbjct: 85602 tgactagtgagatggcctggggaagctgtgaaagaacccaaaagagatcacatactc 85546

Score = 1415 bits (714), Expect = 0.0

Identities = 714/714 (100%)

Strand = Plus / Minus

Query: 1991 tcttgatccacagaaatacatgaaatgtctggtctgtccaccccatcaacaagtcttgaa 2050  
|||||  
Sbjct: 85516 tcttgatccacagaaatacatgaaatgtctggtctgtccaccccatcaacaagtcttgaa 85457

Query: 2051 acaagcaacagatggatagctctgtccaaatggacataagacagacagcagtttcctggt 2110  
|||||  
Sbjct: 85456 acaagcaacagatggatagctctgtccaaatggacataagacagacagcagtttcctggt 85397

Query: 2111 ggtcagggaggggttttggatgatacccaagttattgggatgtcatcttcctggaagcaga 2170  
|||||  
Sbjct: 85396 ggtcagggaggggttttggatgatacccaagttattgggatgtcatcttcctggaagcaga 85337

Query: 2171 gctggggagggagagccatcaccttgataatgggatgaatggaaggaggcttaggacttt 2230  
|||||  
Sbjct: 85336 gctggggagggagagccatcaccttgataatgggatgaatggaaggaggcttaggacttt 85277

Query: 2231 ccactcctggctgagagaggaagagctgcaacggaattaggaagaccaagacacagatca 2290  
|||||  
Sbjct: 85276 ccactcctggctgagagaggaagagctgcaacggaattaggaagaccaagacacagatca 85217

Query: 2291 cccggggcttacttagcctacagatgtcctacgggaacgtgggctggcccagcatagggc 2350  
|||||  
Sbjct: 85216 cccggggcttacttagcctacagatgtcctacgggaacgtgggctggcccagcatagggc 85157

Query: 2351 tagcaaatttgagttggatgattgtttttgctcaaggcaaccagaggaaacttgcataca 2410  
|||||  
Sbjct: 85156 tagcaaatttgagttggatgattgtttttgctcaaggcaaccagaggaaacttgcataca 85097

Query: 2411 gagacagatatactgggagaaatgactttgaaaacctggctctaaggtgggatcactaag 2470  
|||||  
Sbjct: 85096 gagacagatatactgggagaaatgactttgaaaacctggctctaaggtgggatcactaag 85037

Query: 2471 ggatggggcagtcctctgcccaaataaagagaactctggggagcctgagccacaaaaat 2530  
|||||  
Sbjct: 85036 ggatggggcagtcctctgcccaaataaagagaactctggggagcctgagccacaaaaat 84977

Query: 2531 gttcctttattttatgtaaaccctcaagggttatagactgccatgctagacaagcttgtc 2590  
|||||  
Sbjct: 84976 gttcctttattttatgtaaaccctcaagggttatagactgccatgctagacaagcttgtc 84917

Query: 2591 catgtaatattcccatgtttttaccctgccctgccttgattagactcctagcacctggc 2650  
|||||  
Sbjct: 84916 catgtaatattcccatgtttttaccctgccctgccttgattagactcctagcacctggc 84857

Query: 2651 tagtttctaacatgttttgtgcagcacagtttttaataaatgcttgttacattc 2704  
|||||  
Sbjct: 84856 tagtttctaacatgttttgtgcagcacagtttttaataaatgcttgttacattc 84803

Score = 668 bits (337), Expect = 0.0  
Identities = 337/337 (100%)  
Strand = Plus / Minus

Query: 180 ggtgctgctcctctgaagattcaagcttatttcaatgagactgcagacctgccatgcaa 239  
|||||  
Sbjct: 102427 ggtgctgctcctctgaagattcaagcttatttcaatgagactgcagacctgccatgcaa 102368

Query: 240 ttgcaaactctcaaaccacaaagcctgagtgcagctagtagtattttggcaggaccaggaa 299  
|||||  
Sbjct: 102367 ttgcaaactctcaaaccacaaagcctgagtgcagctagtagtattttggcaggaccaggaa 102308

Query: 300 aacttggttctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaag 359  
|||||  
Sbjct: 102307 aacttggttctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaag 102248

Query: 360 tatatgggccgcacaagttttgattcggacagttggaccctgagacttcacaatcttcag 419  
|||||  
Sbjct: 102247 tatatgggccgcacaagttttgattcggacagttggaccctgagacttcacaatcttcag 102188

Query: 420 atcaaggacaagggccttgatcaatgtatcatccatcacaaaaagcccacaggaatgatt 479  
|||||  
Sbjct: 102187 atcaaggacaagggccttgatcaatgtatcatccatcacaaaaagcccacaggaatgatt 102128

Query: 480 cgcattccaccagatgaattctgaactgtcagtgttg 516  
|||||  
Sbjct: 102127 cgcattccaccagatgaattctgaactgtcagtgttg 102091

Score = 595 bits (300), Expect = e-166  
Identities = 303/304 (99%)  
Strand = Plus / Minus

Query: 516 gctaacttcagtcaacctgaaatagtaccaattttctaataaacagaaaatgtgtacata 575  
|||||  
Sbjct: 99741 gctaacttcagtcaacctgaaatagtaccaattttctaataaacagaaaatgtgtacata 99682

Query: 576 aatttgacctgctcatctatacacggttaccagaaacctaaagaagatgagtgttttgcta 635  
|||||

Sbjct: 99681 aatttgacctgctcatctatacacggttaccagaacctaagaagatgagtgttttgcta 99622

Query: 636 agaaccaagaattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtc 695

|||||  
Sbjct: 99621 agaaccaagaattcaactatcgagtatgatggtggtatgcagaaatctcaagataatgtc 99562

Query: 696 acagaactgtacgacggtttccatcagcttgctctgtttcattccctgatgttacgagcaat 755

|||||  
Sbjct: 99561 acagaactgtacgacggtttccatcagcttgctctgtttcattccctgatgttacgagcaat 99502

Query: 756 atgaccatcttctgtattctggaaactgacaagacgcggcttttatcttcacctttctct 815

|||||  
Sbjct: 99501 atgaccatcttctgtattctggaaactgacaagacgcggcttttatcttcacctttctct 99442

Query: 816 atag 819

||||  
Sbjct: 99441 atag 99438

Score = 293 bits (148), Expect = 1e-75

Identities = 148/148 (100%)

Strand = Plus / Minus

Query: 817 tagagcttgaggaccctcagcctccccagaccacattccttggtattacagctgtacttc 876

|||||  
Sbjct: 96676 tagagcttgaggaccctcagcctccccagaccacattccttggtattacagctgtacttc 96617

Query: 877 caacagttattatatgtgtgatgggttttctgtctaatctatggaaatggaagaagaaga 936

|||||  
Sbjct: 96616 caacagttattatatgtgtgatgggttttctgtctaatctatggaaatggaagaagaaga 96557

Query: 937 agcggcctcgcaactcttataaatgtgg 964

|||||  
Sbjct: 96556 agcggcctcgcaactcttataaatgtgg 96529

Score = 258 bits (130), Expect = 6e-65

Identities = 130/130 (100%)

Strand = Plus / Minus

Query: 1 ggaaggcttgacaggggtgaaagctttgcttctctgctgctgtaacagggactagcacag 60

|||||  
Sbjct: 150564 ggaaggcttgacaggggtgaaagctttgcttctctgctgctgtaacagggactagcacag 150505

Query: 61 acacacggatgagtgggggtcatttccagatattaggtcacagcagaagcagccaaaatgg 120

|||||  
Sbjct: 150504 acacacggatgagtgggggtcatttccagatattaggtcacagcagaagcagccaaaatgg 150445

Query: 121 atccccagtg 130  
|||||||  
Sbjct: 150444 atccccagtg 150435

Score = 105 bits (53), Expect = 5e-19  
Identities = 53/53 (100%)  
Strand = Plus / Minus

Query: 130 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggt 182  
|||||||  
Sbjct: 114338 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggt 114286

Score = 93.7 bits (47), Expect = 2e-15  
Identities = 47/47 (100%)  
Strand = Plus / Minus

Query: 963 ggaaccaacacaatggagaggggaagagagtgaacagaccaagaaaag 1009  
|||||||  
Sbjct: 87891 ggaaccaacacaatggagaggggaagagagtgaacagaccaagaaaag 87845

☐ >gi|13650019|gb|AF344861.1|AF344861 Cercopithecus aethiops CD86 protein mRNA, cc  
Length = 1062

Score = 1796 bits (906), Expect = 0.0  
Identities = 1023/1062 (96%)  
Strand = Plus / Plus

Query: 130 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc 189  
|||||||  
Sbjct: 1 gcactatgggactgattaacattctctttgtgatggccttcctgctctctggtgctgctc 60

Query: 190 ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact 249  
| |||||  
Sbjct: 61 ccctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact 120

Query: 250 ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc 309  
|||||||  
Sbjct: 121 ctcaaaaccaaagcctgagtgagctagtagtattttggcagaaccaggaaaacttggttc 180

Query: 310 tgaatgaggtatacttaggcaaagagaaatttgacagtggtcattccaagtatatgggcc 369  
|||||||  
Sbjct: 181 tgaatgaggtatacttaggcaaagagaaatttgacagcggtcattccaagtatatgggcc 240

Query: 370 gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca 429  
|||||||  
Sbjct: 241 gcacaagttttgatccggagagttggaccctgagacttcacaaccttcagatcaaggaca 300



Query: 430 agggcttgatatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacc 489  
|||||  
Sbjct: 301 agggcttgatatcaatgtatcatccatcacaaaaaggcccacaggaatgatccgcatccacc 360

Query: 490 agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaat 549  
|||||  
Sbjct: 361 agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtcccaat 420

Query: 550 ctaatataacagaaaaatgtgtacataaatttgacctgctcatctatacacggttaccag 609  
|||||  
Sbjct: 421 ctaatataacagaaaaatgtgtacataaatttgacctgctcatctatacacggttaccag 480

Query: 610 aacctaagaagatgagtggttttgctaagaaccaagaattcaactatcgagtatgatggta 669  
|||||  
Sbjct: 481 aacctgagaagatgagtggttttgctaagaaccaagaattcaactatcgagtatgatggtg 540

Query: 670 ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgctg 729  
|||||  
Sbjct: 541 ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgctg 600

Query: 730 tttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaaga 789  
|||||  
Sbjct: 601 tttcattccctgatgttacgagcaatatgaccatcttctgtgttctggaaactgacaaga 660

Query: 790 cgcggttttatcttcacctttctctatagagcttgaggaccctcagcctccccagacc 849  
|||  
Sbjct: 661 cacagcttttatcttcacctttctctatagagcttgaggaccctcagcctccccagacc 720

Query: 850 acattcccttggttacagctgtacttccaacagttattatatgtgtgatggttttctgtc 909  
|||||  
Sbjct: 721 acatcccttggttacagctgtacttccaacagttattatatgtgtgatggctttctgtc 780

Query: 910 taattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaacca 969  
|||||  
Sbjct: 781 taattctatggaaatgcaagaagaagaagcagcctcgcaactcttataaacgtggaacca 840

Query: 970 acacaatggagaggaagagagtgaacagaccaagaaaagagaaaaatccatatacctg 1029  
|||||  
Sbjct: 841 acacaatggagaggaagaaagtgaacagaccaaaaaagagaaaaattaatgtacctg 900

Query: 1030 aaagatctgatgaagcccagcgtgttttttaaagttcgaagacatcttcatgcgacaaaa 1089  
|||||  
Sbjct: 901 aaagatctgatgaaaccaatgtgttttttaaagtttgaagacaccttcatgcgacaaaa 960

Query: 1090 gtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttttctaccctt 1149  
|||||  
Sbjct: 961 gtgatacacgtttttaattaaagagtaaagcccatacaagtattcattctttctaccctt 1020

Query: 1150 tcctttgtaagttcctgggcaacctttttgatttcttccaga 1191  
 |||||  
 Sbjct: 1021 tcctttgtaagtttctgggcaacctttttgatttcttccaga 1062

☐ >gi|13650011|gb|AF344857.1|AF344857 Macaca mulatta CD86 protein precursor, mRNA,  
 Length = 1048

Score = 1784 bits (900), Expect = 0.0  
 Identities = 1002/1036 (96%)  
 Strand = Plus / Plus

Query: 129 tgcactatgggactgagtaacattctctttgtgatggccttctgctctctggtgctgct 188  
 |||||  
 Sbjct: 13 tgcactatgggactgagtaacattctctttgtgatggccttctgctctctggtgctgct 72

Query: 189 cctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatgtgcaaac 248  
 ||  
 Sbjct: 73 ccctgaagattcaagcttatttcaatgagactgcagacctgccatgccagtttgcaaac 132

Query: 249 tctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggtt 308  
 |||||  
 Sbjct: 133 tctcaaaaccgaagcctgagtgagctagtagtattttggcagaaccaggaaaacttggtt 192

Query: 309 ctgaatgaggtatacttaggcaaagagaaatttgacagtggtcattccaagtatatgggc 368  
 |||||  
 Sbjct: 193 ctgaatgaggtatacttaggcaaagagaaatttgacagcggtcattccaagtatatgggc 252

Query: 369 cgcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggac 428  
 |||||  
 Sbjct: 253 cgcacaagttttgatccggagagttggaccctgaggcttcacaaccttcagatcaaggac 312

Query: 429 aagggcttgatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccac 488  
 |||||  
 Sbjct: 313 aagggcttgatcaatgtatcatccaccacaaaagcccacaggaatgatccgcatccac 372

Query: 489 cagatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaatt 548  
 |||||  
 Sbjct: 373 cagatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtccaatt 432

Query: 549 tctaataaacagaaaatgtgtacataaatttgacctgctcatctatacacgggttaccca 608  
 |||||  
 Sbjct: 433 tctaataaacagaaaatgtgtacataaatttgacctgctcatctatacacgggttaccca 492

Query: 609 gaacctagaagatgagtggttttgctaagaaccaagaattcaactatcgagtatgatggt 668  
 |||||  
 Sbjct: 493 gaacctgagaagatgagtggttttgctaagaaccaagaattcaactatcgagtatgatggt 552

```

Query: 669 attatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtct 728
      |||
Sbjct: 553 gttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtct 612

Query: 729 gtttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaag 788
      |||
Sbjct: 613 gtttcattccctgatgttacgagcaacatgaccatcttctgtgttctggaaactgacaag 672

Query: 789 acgcggtttttatcttcacctttctctatagagcttgaggaccctcagcctccccagac 848
      |||
Sbjct: 673 acacagctttttatcttcacctttctctatagagcttgaggaccctcagcctccccagac 732

Query: 849 cacattccttggttacagctgtacttccaacagttattatatgtgtgatgggttttctgt 908
      |||
Sbjct: 733 cacatcccttggttacagctgtacttccaacagttattatatgtgtgatgggttttctgt 792

Query: 909 ctaattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaacc 968
      |||
Sbjct: 793 ctaattctatggaaatggaagaagaagaagcagcctcgcaactcttataaatgtggaacc 852

Query: 969 aacacaatggagaggggaagagagtgaacagaccaagaaaagagaaaaatccatatacct 1028
      |||
Sbjct: 853 aacacaatggagaggggaagagagtgaacagaccaaaaaagagaaaaattaatgtacct 912

Query: 1029 gaaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaa 1088
      |||
Sbjct: 913 gaaagatctgatgaagcccaatgtgtttttaaaagtttgaagacaccttcatgcgacaaa 972

Query: 1089 agtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttttctaccct 1148
      |||
Sbjct: 973 agtgatacacgtttttaattaaagagtaaagcccatacaagtattcattctttctaccct 1032

Query: 1149 ttcctttgtaagttcc 1164
      |||
Sbjct: 1033 ttcctttgtaagttcc 1048

```

☐ >gi|13650000|gb|AF344840.1|AF344840 Cercocebus torquatus atys CD86 protein prec  
Length = 1062

Score = 1780 bits (898), Expect = 0.0  
Identities = 1021/1062 (96%)  
Strand = Plus / Plus

```

Query: 130 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc 189
      |||
Sbjct: 1 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc 60

Query: 190 ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact 249

```

7/9/2004

Sbjct: 781 |||||  
taattctatggaaatggaagaagaagaagcagcctcgcaactcttataactgtggaacca 840

Query: 970 acacaatggagaggggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctg 1029  
|||||

Sbjct: 841 acacaatggagaggggaagagagtgaacagaccaaaaaagagaaaaaattaatgtacctg 900

Query: 1030 aaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaa 1089  
|||||

Sbjct: 901 aaagatctgatgaagcccaatgtgtttttaaaagtttgaagacaccttcatgcgacaaaa 960

Query: 1090 gtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttttctaccctt 1149  
|||||

Sbjct: 961 gtgatacgcattttttaattaaagagtaaagcccatacaagtattcattctttctaccctt 1020

Query: 1150 tcctttgtaagttcctgggcaacctttttgatttcttcaga 1191  
|||||

Sbjct: 1021 tcctttgtaagtttctgggcaacctttttgatttcttcaga 1062

☐ >gi|13655490|gb|AF344851.1|AF344851 Macaca nemestrina CD86 protein precursor, mRNA  
Length = 1044

Score = 1721 bits (868), Expect = 0.0  
Identities = 994/1036 (95%)  
Strand = Plus / Plus

Query: 130 gcactatgggactgagtaacattctctttgtgatggccttctgctctctggtgctgctc 189  
|||||

Sbjct: 1 gcactatgggactgagtaacattctctttgtgatggccttctgctctctggtgctgctc 60

Query: 190 ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatgttgcaaact 249  
| |||||

Sbjct: 61 ccctgaagattcaagcttacttcaatgagactgcagacctgccatgccagtttgcaaact 120

Query: 250 ctcaaaaccaaagcctgagtgaagctagtagtattttggcaggaccaggaaaacttggttc 309  
|||||

Sbjct: 121 ctcaaaaccgaagcctgagtgaagctagtagtattttggcagaaccaggaaaacttggttc 180

Query: 310 tgaatgaggtatacttaggcaaagagaaatttgacagtggttcattccaagtatatgggcc 369  
|||||

Sbjct: 181 tgaatgaggtatacttaggcaaagagaaatttgacagcgttcattccaagtatatgggcc 240

Query: 370 gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca 429  
|||||

Sbjct: 241 gcacaagatttgatccggagagttggaccctgaggcttcgcaaccttcagatcaaggaca 300

Query: 430 agggcttgatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacc 489  
|||||

Sbjct: 301 agggcttgatatcaatgtatcatccaccacaaaaggccacaggaatgatccgcatccacc 360

Query: 490 agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaattt 549  
|||||

Sbjct: 361 agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtcccaattt 420

Query: 550 ctaatataacagaaaaatgtgtacataaatttgacctgctcatctatacacggttaccag 609  
|||||

Sbjct: 421 ctaatataacagaaaaatgtgtacataaatttgacctgctcatctatacacggttaccag 480

Query: 610 aacctaagaagatgagtggttttgctaagaaccaagaattcaactatcgagtatgatggta 669  
|||||

Sbjct: 481 aacctgagaagatgagtggttttgctaagaaccaagaattcaactatcgagtatgatggtg 540

Query: 670 ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgctg 729  
|||||

Sbjct: 541 ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgctg 600

Query: 730 tttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaaga 789  
|||||

Sbjct: 601 tttcattccctgatgttacgagcaacatgaccatcttctgtgttctggaaactgacaaga 660

Query: 790 cgcggttttatcttcacctttctctatagagcttgaggaccctcagcctccccagacc 849  
|||

Sbjct: 661 cacagcttttatcctcacctttctctatagagcttgaggaccctcagcctccccagacc 720

Query: 850 acattccttggtattacagctgtacttccaacagttattatatgtgtgatggttttctgtc 909  
|||

Sbjct: 721 acatcccttggtattacagctgtacttccatcagttgttatatgtgtgatggctttctgtc 780

Query: 910 taattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaacca 969  
|||||

Sbjct: 781 taattctatggaagtggaagaagaagaagcaacctcgcaactcttataaatgtggaacca 840

Query: 970 acacaatggagaggggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctg 1029  
|||||

Sbjct: 841 acacaatggagaggggaagagagtgaacagaccaaaaaaagagaaaaattaatgtacctg 900

Query: 1030 aaagatctgatgaagcccagcgtgttttttaaagttcgaagacatcttcacgacaaaa 1089  
|||||

Sbjct: 901 aaagatctgatgaagcccaatgtgttttttaaagtttgaagacaccttcacgacaaaa 960

Query: 1090 gtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttttctaccctt 1149  
|||||

Sbjct: 961 gtgatacacgtttttaattaaagagtaaagcccatacaagtattcattctttttaccctt 1020

Query: 1150 tcctttgtaagttcct 1165  
|||||

Sbjct: 1021 tcctttgtaagttcct 1036

☐ >gi|13649983|gb|AF344836.1|AF344836 Papio cynocephalus anubis CD86 protein prec  
cds  
Length = 901

Score = 1179 bits (595), Expect = 0.0  
Identities = 667/691 (96%)  
Strand = Plus / Plus

Query: 129 tgcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgct 188  
|||||  
Sbjct: 1 tgcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgct 60

Query: 189 cctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaac 248  
||  
Sbjct: 61 ccctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaac 120

Query: 249 tctcaaaaccaaagcctgagttagtagtagtattttggcaggaccaggaaaacttggtt 308  
|||||  
Sbjct: 121 tctcaaaaccaaagcctgagttagtagtagtattttggcagaatcaggaaaacttggtt 180

Query: 309 ctgaatgaggtatacttaggcaaagagaaatttgacagtggttcattccaagtatatgggc 368  
|||||  
Sbjct: 181 ctgaatgaggtatacttaggcagagaaaaatttgacagcggttcattccaagtatatgggc 240

Query: 369 cgcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggac 428  
|||||  
Sbjct: 241 cgcacaagttttgatccggagagttggaccctgaggcttcacaaccttcagatcaaggac 300

Query: 429 aagggttgatcaatgtatcatccatcacaaaaggccacaggaatgattcgcatccac 488  
|||||  
Sbjct: 301 aagggttgatcaatgtatcatccatcacaaaaggccacaggaatgatccgcatccac 360

Query: 489 cagatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaatt 548  
|||||  
Sbjct: 361 cagatgaattctgaactgtcagtgcttgctagcttcagtcaacctgaaatagtccaatt 420

Query: 549 tctaataataacagaaaatgtgtacataaatttgacctgctcatctatacacggttaccca 608  
|||||  
Sbjct: 421 tctaataataacagaaaatgtgtacataaatttgacctgctcatctatacacggttaccca 480

Query: 609 gaacctaagaagatgagtggttttgctaagaaccaagaattcaactatcgagtatgatggt 668  
|||||  
Sbjct: 481 gaacctgagaagatgagtggttttgctaagaaccaagaattcaactatcgagtatgatggt 540

Query: 669 attatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgctt 728  
|||||

Sbjct: 541 gttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtct 600

Query: 729 gtttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaag 788

|||||  
Sbjct: 601 gtttcattccctgatgttacgagcaacatgaccatcttctgtgttctggaaactgacaag 660

Query: 789 acgcggttttatcttcacctttctctatag 819

|||  
Sbjct: 661 acacagcttttatcctcacctttctctatag 691

Score = 307 bits (155), Expect = 7e-80

Identities = 191/203 (94%)

Strand = Plus / Plus

Query: 963 ggaaccaacacaatggagaggggaagagagtgaacagaccaagaaaagagaaaaaatccat 1022

|||||  
Sbjct: 691 ggaaccaacacaatggagaggggaagagagtgaacagacaaaaaagagaaaaattaat 750

Query: 1023 atacctgaaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgc 1082

|||||  
Sbjct: 751 gtacctgaaagatctgatgaagcccaatgtgtttttaaaagtttgaagacaccttcatgc 810

Query: 1083 gacaaaagtatacatgtttttaattaaagagtaaagcccatatacaagtattcattttttc 1142

|||||  
Sbjct: 811 gacaaaagtatacatgtttttaattaaagagtaaagcccatatacaagtattcattctttc 870

Query: 1143 taccctttcctttgtaagttcct 1165

|||||  
Sbjct: 871 taccctttcctttgtaagttcct 893

☐ >gi|808032|gb|U17722.1|HSB72S8 ☒ Human CTLA-4 counter-receptor B7.2 (B7.2) gene,  
cds

Length = 630

Score = 805 bits (406), Expect = 0.0

Identities = 409/410 (99%)

Strand = Plus / Plus

Query: 1008 agagaaaaaatccatatacctgaaagatctgatgaagcccagcgtgtttttaaaagttcg 1067

|||||  
Sbjct: 221 agagaaaaaatccatatacctgaaagatctgatgaagcccagcgtgtttttaaaagttcg 280

Query: 1068 aagacatcttcatgcgacaaaagtatacatgtttttaattaaagagtaaagcccatata 1127

|||||  
Sbjct: 281 aagacatcttcatgcgacaaaagtatacatgtttttaattaaagagtaaagcccatata 340

Query: 1128 agtattcattttttctaccctttcctttgtaagttcctgggcaacctttttgatttcttc 1187



```
|||||
Sbjct: 341 agtattcattttttctaccctttcctttgtaagttcctgggcaacctttttgatttcttc 400

Query: 1188 cagaaggcaaaaagacattaccatgagtaataagggggctccaggactccctctaagtgg 1247
|||||
Sbjct: 401 cagaaggcaaaaagacattaccatgagtaataagggggctccaggactccctctaagtgg 460

Query: 1248 aatagcctccctgtaactccagctctgctccgtatgccaagaggagactttaattctctt 1307
|||||
Sbjct: 461 aatagcctccctgtaactccagctctgctccgtatgacaagaggagactttaattctctt 520

Query: 1308 actgcttcttttcacttcagagcacacttatgggccaagcccagcttaatggctcatgac 1367
|||||
Sbjct: 521 actgcttcttttcacttcagagcacacttatgggccaagcccagcttaatggctcatgac 580

Query: 1368 ctggaaataaaaatttaggaccaatacctcctccagatcagattcttctct 1417
|||||
Sbjct: 581 ctggaaataaaaatttaggaccaatacctcctccagatcagattcttctct 630
```

☐ >gi|808028|gb|U17718.1|HSB72S4 Human CTLA-4 counter-receptor B7.2 (B7.2) gene, ε  
Length = 741

Score = 660 bits (333), Expect = 0.0  
Identities = 336/337 (99%)  
Strand = Plus / Plus

```
Query: 180 ggtgctgctcctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaa 239
|||||
Sbjct: 240 ggtgctgctcctctggagattcaagcttatttcaatgagactgcagacctgccatgccaa 299

Query: 240 ttgcaaactctcaaaaccaaagcctgagttagtagtagtattttggcaggaccaggaa 299
|||||
Sbjct: 300 ttgcaaactctcaaaaccaaagcctgagttagtagtagtattttggcaggaccaggaa 359

Query: 300 aacttggttctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaag 359
|||||
Sbjct: 360 aacttggttctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaag 419

Query: 360 tatatgggccgcacaagttttgattcggacagttggaccctgagacttcacaatcttcag 419
|||||
Sbjct: 420 tatatgggccgcacaagttttgattcggacagttggaccctgagacttcacaatcttcag 479

Query: 420 atcaaggacaaggccttgatcaatgtatcatccatcacaaaagcccacaggaatgatt 479
|||||
Sbjct: 480 atcaaggacaaggccttgatcaatgtatcatccatcacaaaagcccacaggaatgatt 539

Query: 480 cgcattccaccagatgaattctgaactgtcagtgcttg 516
|||||
```

Sbjct: 540 cgcattccaccagatgaattctgaactgtcagtgcttg 576

☐ >gi|808029|gb|U17719.1|HSB72S5 Human CTLA-4 counter-receptor B7.2 (B7.2) gene, ε  
Length = 737

Score = 603 bits (304), Expect = e-169  
Identities = 304/304 (100%)  
Strand = Plus / Plus

Query: 516 gctaacttcagtcaacctgaaatagtaccaatttctaataaacagaaaatgtgtacata 575  
|||||  
Sbjct: 151 gctaacttcagtcaacctgaaatagtaccaatttctaataaacagaaaatgtgtacata 210

Query: 576 aatttgacctgctcatctatacacggttaccagaacctagaagatgagtgttttgcta 635  
|||||  
Sbjct: 211 aatttgacctgctcatctatacacggttaccagaacctagaagatgagtgttttgcta 270

Query: 636 agaaccaagaattcaactatcgagtatgatggattatgcagaaatctcaagataatgtc 695  
|||||  
Sbjct: 271 agaaccaagaattcaactatcgagtatgatggattatgcagaaatctcaagataatgtc 330

Query: 696 acagaactgtacgacgtttccatcagcttgctgtttcattccctgatgttacgagcaat 755  
|||||  
Sbjct: 331 acagaactgtacgacgtttccatcagcttgctgtttcattccctgatgttacgagcaat 390

Query: 756 atgaccatcttctgtattctggaaactgacaagacgcggccttttatcttcacctttctct 815  
|||||  
Sbjct: 391 atgaccatcttctgtattctggaaactgacaagacgcggccttttatcttcacctttctct 450

Query: 816 atag 819  
|||  
Sbjct: 451 atag 454

☐ >gi|6572518|gb|AF106827.1|AF106827 ☒ Canis familiaris truncated B7-2 protein (CI  
Length = 1795

Score = 396 bits (200), Expect = e-106  
Identities = 502/602 (83%), Gaps = 3/602 (0%)  
Strand = Plus / Plus

Query: 129 tgcactatgggactgagtaacattctctttgtgatggccttcctgctctctgggtgctgct 188  
|||||  
Sbjct: 19 tgcactatggaactgaataacattctctttgtgatgaccctcctgctctatgggtgctgct 78

Query: 189 cctctgaagattcaagcttattttcaatgagactgcagacctgccatgccaatttgcaaac 248  
| |||||  
Sbjct: 79 tccatgaagagtcaagcatattttcaacaagactggagaactgccatgccattttacaaat 138

Query: 249 tctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggtt 308  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 139 tctcaaaacataagcctggatgagttggttagtgttttggcaggaccaggataagctggtt 198

Query: 309 ctgaatgaggtatacttaggcaaagagaaatttgacagtggttcattccaagtatatgggc 368  
||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 199 ctgtacgagctatacagaggcaaagagaaccctcaaaatgttcacgcaagtataagggc 258

Query: 369 cgcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggac 428  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 259 cgcacaagctttgacaaagacaattggaccctgagactccataatattcagatcaaggac 318

Query: 429 aagggcttgtatcaatgtatcatccatcacaaaaagccacaggaatgattcgcatccac 488  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 319 aagggcttgtatcaatgtttcgttcatcataaagggcccaaaggactcgttcccatgcac 378

Query: 489 cagatgaattctgaactgtcagtgcttgtaacttcagtcaacctgaaatagtaccaatt 548  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 379 cagatgaattctgacctatcagtgcttgtaacttcagtcaacctgaaataatggtaact 438

Query: 549 tctaataataacagaaaa---tgtgtacataaatttgacctgctcatctatacacggttac 605  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 439 tctaataagaacagaaaattctggcatcataaatttgacctgctcatccatacaaggttac 498

Query: 606 ccagaacctaaagaagatgagtggttttgtaagaaccaagaattcaactatcgagtatgat 665  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 499 ccagaaccaaggagatgtatttttggtaaaaaccgagaattcaagtactaagtatgat 558

Query: 666 ggtattatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttg 725  
|| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 559 actgtcatgaagaaatctcaaaataatgtcacagaactctacaacgtttctatcagcttg 618

Query: 726 tc 727  
||  
Sbjct: 619 tc 620

Score = 67.9 bits (34), Expect = 1e-07  
Identities = 81/96 (84%), Gaps = 3/96 (3%)  
Strand = Plus / Plus

Query: 1029 gaaagatctgatgaagcccagcgtgttttttaaagttcgaagacatcttcagcgacaaa 1088  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 775 gaaagatctgatgaagcccagtggtg---ttaacatttcgaagacagcttcaggcgacaac 831

Query: 1089 agtgatacatgtttttaattaaagagtaaagcccat 1124  
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Sbjct: 832 agtactacacagttttaattaaagagtaaagtccat 867

Score = 60.0 bits (30), Expect = 3e-05  
Identities = 169/210 (80%), Gaps = 9/210 (4%)  
Strand = Plus / Plus

Query: 1537 actacctcctcagtcctgggtgggacttatgtat-ttatgaccttatagtgtt-----aat 1590  
||||||| ||||||||| || ||||| ||||| | ||||||||| |||  
Sbjct: 1250 actacctctgcagtcctgggtgggagttttgtatgttatggctttatagtgttgctttaat 1309

Query: 1591 atcttgaaacatagagatctatgtactgtaatagtgtgattactatgctctagagaaaag 1650  
|| |||| ||||| ||| | |||||| ||||| ||| |||||||  
Sbjct: 1310 attttgagacataaaagagatgtgtactataataatgtaattactatgccct-gagaaaat 1368

Query: 1651 tctaccc-ctgctaaggagttctcatccctctgtcagggtcagtaaggaaaacgggtggcc 1709  
||||||| ||||| ||||| ||| |||||| ||||||||| ||||| |||||  
Sbjct: 1369 tctaccactgctgaggagctcttgctcctctgtgagggtcagtacg-aaaatgggtggct 1427

Query: 1710 tagggtacaggcaacaatgagcagaccaac 1739  
| | | | | ||||||||| |||||  
Sbjct: 1428 tgggtgctgacaacaatgagcagaccaac 1457

Score = 58.0 bits (29), Expect = 1e-04  
Identities = 32/33 (96%)  
Strand = Plus / Plus

Query: 1776 cctggagccacttctatctgggctgttgctaata 1808  
||||||||||| ||||||||| |||||  
Sbjct: 1506 cctggagccacttctatctgggctgctgctaata 1538

Score = 50.1 bits (25), Expect = 0.026  
Identities = 34/37 (91%)  
Strand = Plus / Plus

Query: 1308 actgcttcttttcacttcagagcacacttatgggcca 1344  
||||||||||| ||||||||| |||||  
Sbjct: 1029 actgcttcttttcacttcagagcacacttggtgggcca 1065

☐ >gi|6572516|gb|AF106826.1|AF106826 **LUG** Canis familiaris B7-2 protein (CD86) mF  
Length = 1897

Score = 396 bits (200), Expect = e-106  
Identities = 502/602 (83%), Gaps = 3/602 (0%)  
Strand = Plus / Plus

Score = 75.8 bits (38), Expect = 5e-10  
Identities = 157/196 (80%), Gaps = 3/196 (1%)  
Strand = Plus / Plus

7/9/2004

Identities = 34/37 (91%)

Strand = Plus / Plus

Query: 1308 actgcttcttttctacttcagagcacacttatgggcca 1344

|||||

Sbjct: 1175 actgcttcttttcatctcagagcacacttgaggcca 1211

☐ >gi|5381423|gb|AF157827.1|AF157827 Felis catus CD86 antigen (CD86) mRNA, complet  
Length = 1138

Score = 361 bits (182), Expect = 5e-96

Identities = 508/616 (82%), Gaps = 3/616 (0%)

Strand = Plus / Plus

Query: 130 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc 189

|||||

Sbjct: 79 gcactatgggactgagtcacactctccttgatggccttcctgctctctggtggttctt 138

Query: 190 ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatgtgcaaact 249

| |||||

Sbjct: 139 ccatgaagagtcaagcatatttcaacaagactggagaactgccatgccattttacaaact 198

Query: 250 ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc 309

|||||

Sbjct: 199 ctcaaaacataagcctggatgagctggtagtagtattttggcaggaccaggataagctggttc 258

Query: 310 tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatggggc 369

|| |||||

Sbjct: 259 tgtatgagatattcagaggcaaagagaacctcaaatgttcattctcaaatataagggc 318

Query: 370 gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca 429

| |||||

Sbjct: 319 gtacaagctttgacaaggacaactggaccctgagactccacaatgttcagatcaaggaca 378

Query: 430 agggccttgatcaatgtatcatccatcacaaaaagccacaggaatgattcgcatccacc 489

|||||

Sbjct: 379 agggcacatatcactgtttcattcattataaagggcccaaaggactagttcccatgcacc 438

Query: 490 agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtagtaattt 549

| |||||

Sbjct: 439 aaatgagttctgacctatcagtgcttgctaacttcagtcaacctgaaataacagtaactt 498

Query: 550 ctaatataacagaaaa---tgtgtacataaatttgacctgctcatctatacacggttacc 606

|||||

Sbjct: 499 ctaatagaacagaaaattctggcatcataaatttgacctgctcatctatacaagggttacc 558

Query: 607 cagaacctaagaagatgagtggttttgctaagaaccaagaattcaactatcgagtatgatg 666

|||||

7/9/2004





Query: 929 gaagaagaagcggcctcgcaactcttataaatgtggaaccaacacaatggagaggggaaga 988  
 |||||  
 Sbict: 1003 gaagaagaagcagcctggccctctcatgaatgtgaaaccatcaaaggagagaaaaaga 1062

Query: 989    gagtgaacagaccaagaaaagagaaaaaatccatatacctgaaagatctgatgaagccca    1048  
             ||| ||||| ||||| ||||| ||| ||| ||||| ||||| ||||| |||||  
Sbjct: 1063    gagcaaacagaccaacgaaagagtaccataccacgtacctgagagatctgatgaagccca    1122

```
Query: 1049 gcgtgttttttaaagattcgaagacatcttcatgcgacaaaagtgtacatgtttttaatt 1108
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Spict: 1123 gtgtatt---aacattttgaagacagcctcagcgacaaaagtactacacatttttaatt 1179
```

```
Query: 1109 aaagagtaaagcccata 1125
      ||||| ||||| |||||
Sbjct: 1180 aaagaataaagtccata 1196
```

Score = 50.1 bits (25), Expect = 0.026  
Identities = 46/53 (86%)  
Strand = Plus / Plus

Query: 1586 ttaatatcttgaacatagagatctatgtactgtaatagtgtgattactatgc 1638  
 |||  
 Spict: 1644 ttaatatcttgaacataaagagatgtgtactataataatgtaattactatgc 1696

```

☐ >gi|9796387|dbj|AB030652.1|    Felis catus mRNA for B-lymphocyte activation antigen
                                complete cds
                                Length = 1270

```

Score = 361 bits (182), Expect = 5e-96  
Identities = 508/616 (82%), Gaps = 3/616 (0%)  
Strand = Plus / Plus

Query: 130 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc 189  
 |||||  
 Sbjct: 256 gcactatgggactgagtcacactctccttgtgatggccttcctgctctctgggtttctt 315

Query: 190 ctctgaagattcaagcttattttcaatgagactgcagacctgccatgccaatgtgcaaact 249  
| | | | | | | | | | | | | | | | | | | | | | | | |  
Sbjct: 316 ccatgaagaagtcaagcatattttcaacaagactggagaactgccatgccattttacaaact 375

Query: 250 ctcaaaaccaaagcctgagttagttagtatattttggcaggaccaggaaaacttggttc 309  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 376 ctcaaaacataagcctggatgagctggtagtatattttggcaggaccaggataagctgggttc 435

Query: 310 tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcc 369  
 || ||||| ||| | ||||| ||||| | | ||||| ||||| ||||| |||||  
 Sbjct: 436 tgtatgagatattcagaggcaaagagaaccctcaaatgttcatctcaaatataagggcc 495

Query: 370 gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca 429  
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 496 gtacaagctttgacaaggacaactggaccctgagactccacaatgttcagatcaaggaca 555

Query: 430 agggccttgatcaatgtatcatccatcacaaaaagccacaggaatgattcgcatccacc 489  
 ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 556 agggcacatatcactgtttcattcattataaagggcccaaaggactagttcccatgcacc 615

Query: 490 agatgaattctgaactgtcagtgcttgctaacttcagtcacactgaaatagtaccaattt 549  
 | ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 616 aaatgagttctgacctatcagtgcttgctaacttcagtcacactgaaataacagtaactt 675

Query: 550 ctaatataacagaaaa---tgtgtacataaatttgacctgctcatctatacacggttacc 606  
 ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 676 ctaatagaacagaaaattctggcatcataaatttgacctgctcatctatacaaggttacc 735

Query: 607 cagaacctaagaagatgagtggttttgctaagaaccaagaattcaactatcgagtatgatg 666  
 ||||| ||||| ||||| || ||||| || ||||| ||||| ||||| ||||| |||||  
 Sbjct: 736 cagaacctaaggagatgtattttcagctaaacactgagaattcaactactaagtatgata 795

Query: 667 gtattatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgt 726  
 | | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 796 ctgtcatgaagaaatctcaaaataatgtgacagaactgtacaacgtttctatcagcttgc 855

Query: 727 ctgtttcattccctga 742  
 || ||||| |||||  
 Sbjct: 856 ctttttcagtcctga 871

Score = 69.9 bits (35), Expect = 3e-08  
 Identities = 157/197 (79%), Gaps = 3/197 (1%)  
 Strand = Plus / Plus

Query: 929 gaagaagaagcggcctcgcaactcttataaatgtggaaccaacacaatggagaggggaaga 988  
 ||||| ||||| ||||| || ||||| ||||| || ||||| ||||| ||||| |||||  
 Sbjct: 1064 gaagaagaagcagcctggccctctcatgaatgtgaaaccatcaaaggagagaaaaaga 1123

Query: 989 gagtgaacagaccaagaaaaagagaaaaaatccatatacctgaaagatctgatgaagccca 1048  
 ||| ||||| ||||| ||||| | | ||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 1124 gagcaaacagaccaacgaaagagtaccataccacgtacctgagagatctgatgaagccca 1183

Query: 1049 gcgtgttttttaaaagttcgaagacatcttcatgcgacaaaagtatacatgtttttaatt 1108  
 | ||| ||||| || ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 1184 gtgtg---ttaacattttgaagacagcctcaggcgacaaaagtactacacatttttaatt 1240

Query: 1109 aaagagtaaagcccata 1125

\_\_\_\_\_

Sbjct: 1241 aaagaataaaagtccata 1257

□>gi|755098|dbj|D49842.1|RABCD86B Oryctolagus cuniculus mRNA for CD86, complete c

Length = 1156

Score = 355 bits (179), Expect = 3e-94

Identities = 493/595 (82%), Gaps = 2/595 (0%)

Strand = Plus / Plus

Query: 129 tgcactatgggactgagtaacattctctttgtgatggccttcctgctctctgggtgctgct 188

XXXXXXXXXXXX

Sbjct: 19 tgcacaatgggactgagtgtcacggtctttgtgatggccctcctgctctctggtgctgct 78

Query: 189 cctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaat ttgcaaac 248

Sbjct: 79 tcccttaggatacaggcttatttcaacaagactgcagacctgccatgccagttttacaaac 138

Query: 249 tctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttgggtt 308

\_\_\_\_\_

Sbjct: 139 tctcaaagcagaagcctaagtgagctggtagtattttggcaggaccaggagaggttgggtt 198

Query: 309 ctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggc 368

[illegible]

Sbjct: 199 ctgtacgagctcttcttaggcagagagaaaacctgacaatgtggatcctaagtacattggc 258

Query: 369 cgcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggac 428

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Sbjct: 259 cgcacaagctttgaccaggaaagttggaacctacaacttcacaacgttcagatcaaggac 318

Query: 429 aagggcttgatatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcattccac 488

[illegible]

Sbjct: 319 aagggcgtgtatcaatgttttgtccatcacagaggggccaagggctggttcccatctac 378

Query: 489 cagatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtagccaatt 548

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Sbjct: 379 cagatgaattctgagctgtcagtgcttgctaatttcactcaaccggaaataacattaatt 438

Query: 549 tctaataataaca-gaaaatgtgtacataaatttgacctgctcatctatacacggttaccc 607

$\frac{1}{2} \quad \frac{1}{2} \quad \frac{1}{2}$

Sbjct: 439 tccaatataacaagaaattctgc-cataaatttgacctgctcgtctgtacaaggctaccc 497

Query: 608 agaacctaagaagatgagtgttttgctaagaaccaagaattcaactatcgagtatgatgg 667

[illegible]

Sbjct: 498 agaacctaagaagatgttctttgtgctaaaaactgagaatgcaaccactgagtatgatgg 557

Query: 668 tattatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagc 722  
| | | | |  
Sbjct: 558 tgtcatcgagaaatctcaagataatgtcacaggactgtacaacatttccatcagc 612

☐ >gi|808030|gb|U17720.1|HSB72S6 Human CTLA-4 counter-receptor B7.2 (B7.2) gene, cDNA  
Length = 571

Score = 293 bits (148), Expect = 1e-75  
Identities = 148/148 (100%)  
Strand = Plus / Plus

```
Query: 817 tagagcttgaggacctcagcctccccagaccacattccttggattacagctgtacttc 876
      |||
Sbjct: 167 tagagcttgaggacctcagcctccccagaccacattccttggattacagctgtacttc 226
```

Query: 877 caacagttattatatgtgtgatggttttctgtctaattctatggaaatggaagaagaaga 936  
 |||||  
 Sbict: 227 caacagttattatatgtgtgatggttttctgtctaattctatggaaatggaagaagaaga 286

```

Query: 937 agcggcctcgcaactcttataaatgtgg 964
      |||
Sbjct: 287 agcggcctcgcaactcttataaatgtgg 314

```

□ >[gi|47523527|ref|NM\\_214222.1](#) **LU** Sus scrofa CD86 protein (CD86), mRNA  
Length = 994

Score = 264 bits (133), Expect = 9e-67  
Identities = 398/481 (82%), Gaps = 4/481 (0%)  
Strand = Plus / Plus

```
Query: 135 atgggactgagtaacattctctttgtgatggccttctctgctctctgggtctg-ctcctct 193
          |||
Sbjct: 1 atgggactgagtaacattctctttgtgatggccttctctgctctctgggtctgctcctct-t 59
```

```
Query: 194  gaagattcaagcttatttcaatgagactgcagacctgccatgccaatgtgcaaactctca 253
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 60   gaaaagtcaggcatatttcaatgagactggagaactgccgtgccattttacaaactcgca 119
```

Query: 254 aaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaa 313  
 ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 120 gaacctaagcctggatgagctggatcatattttggcaggaccaggataaacctggttctcta 179

Query: 314 tgagggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcac 373  
 ||| |||| |||| |||| ||| | ||| |||| |||| |||| |||| |||| ||||  
 Sbjct: 180 cgagctataccgaggccaagagaagcctcataatgttaattccaagtatatgggtcgcac 239

7/9/2004

7/9/2004

Sbjct: 246 gaactggtgatattttggcaggatcagaataagttggttctttatgagctattcaaaggc 305

Query: 330 aaagagaaatttgacagtgttcattccaagtatatgggccgcacaagttttgattcggac 389  
 ||||| | | ||| | | ||||| | | ||||| | | ||||| | | ||||| | |

Sbjct: 306 caagagaagcccaataatgttaatcccaagtatataggccgcacaagctttgaccaggac 365

Query: 390 agttggaccctgagacttcacaatcttcagatcaaggacaagggcttgatcaatgtatc 449  
 ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | |

Sbjct: 366 agttggaccttgagactccacaacggtcaaatacaagacacaggctcgtatcaatgtttc 425

Query: 450 atccatcacaaaaagcccacaggaatgattcgcatccaccagatgaattctgaactgtca 509  
 ||||| | | || | | | ||||| | | ||||| | | ||||| | | ||||| | |

Sbjct: 426 atccatcatagaaggtcccaaggattggtttccatccaccagatgagttctgacctgata 485

Query: 510 gtgcttgctaacttcagtcaacctgaaatagtaccaatttctaataaacagaaaaatgtg 569  
 ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | |

Sbjct: 486 gtgctggctaacttcagtcaaccagaaataagactaattgctaaccaaacagaaaa-gtc 544

Query: 570 ta----cataaatttgacctgctcatctatacacggttaccagaaacctaagaagatg 623  
 || | | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | |

Sbjct: 545 taacatcatcaatttgacctgctcatctatacaagggttaccagaaacctcagaggatg 602

Score = 42.1 bits (21), Expect = 6.3

Identities = 45/53 (84%)

Strand = Plus / Plus

Query: 676 agaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtct 728  
 ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | |

Sbjct: 655 agaaatctcaaagtaatatcacagaactatacaatgtttctatcagcgtgtct 707

☐ >gi|40217708|gb|AC117662.13| ☒ Mus musculus chromosome 16, clone RP23-351D19, cc  
 Length = 293822

Score = 143 bits (72), Expect = 2e-30

Identities = 198/240 (82%)

Strand = Plus / Minus

Query: 201 caagcttatttcaatgagactgcagacctgccatgccaatgtgcaaactctcaaaaccaa 260  
 ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | |

Sbjct: 100828 caagcttatttcaatgggactgcataatctgccgtgccatttacaaagggtcaaaacata 100769

Query: 261 agcctgagttagcttagtagtattttggcaggaccaggaaaacttggttctgaatgaggtta 320  
 ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | |

Sbjct: 100768 agcctgagttagctggttagtagtattttggcaggaccaggaaaagttggttctgtacgagcac 100709

Query: 321 tacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcacaagtttt 380  
 || | | ||||| | | ||||| | | ||||| | | ||||| | | ||||| | |



Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgat 440  
|| ||| ||| || | ||||||||| ||||||||| |||||||||  
Sbjct: 100648 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgat 100589

Query: 645 aattcaactatcgagtatgatggattatgcagaaatctcaagataatgtcacagaactg 704  
 |||||  
 Sbjct: 98313 aattcaactaatgagtatgggtgataacatgcagatatcacaagataatgtcacagaactg 98254

```

Query: 705      t 705
        |
Sbjct: 98253    t 98253

```

Score = 143 bits (72), Expect = 2e-30  
Identities = 198/240 (82%)  
Strand = Plus / Plus

```
Query: 201 caagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaaaaccaa 260
          |||||
Sbjct: 117 caagcttatttcaatgggactgcatactgccgtgccatttacaaggctcaaaacata 176
```

```
Query: 261 agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320
          |||||
Sbjct: 177 agcctgagtgagctggttagtattttggcaggaccagcaaaagttggttctgtacgagcac 236
```

Query: 321 tacttaggc~~aag~~~~aga~~~~aa~~tattgacagtgttcattccaagtatatgggccgcacaagtttt 380  
 . |||||  
 Sbjct: 237 tatttgccacagagaaaacttgatagtgtgaatgccaa~~gtac~~cctgggccgcacga~~gctt~~ 296

Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggttgat 440  
|| ||| |||| | | ||||||| ||||||| ||||||| ||||||| |||||||  
Sbjct: 297 gagaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggtcgat 356

Score = 58.0 bits (29), Expect = 1e-04  
Identities = 53/61 (86%)  
Strand = Plus / Plus

7/9/2004

||||| ||||| || || ||||| ||| ||||| ||||| |||||  
Sbjct: 555 aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 614

Query: 705 t 705

|  
Sbjct: 615 t 615

Score = 46.1 bits (23), Expect = 0.41

Identities = 35/39 (89%)

Strand = Plus / Plus

Query: 501 gaactgtcagtgccttgctaacttcagtcaacctgaaata 539

||||| ||||| || || ||||| ||||| |||||  
Sbjct: 417 gaactgtcagtgccttgctaacttcagtgaacctgaaata 455

☐ >gi|4587843|gb|AF065899.1|AF065899 **LUG** Mus musculus strain B10.S/J CD86 antigen  
Length = 984

Score = 143 bits (72), Expect = 2e-30

Identities = 198/240 (82%)

Strand = Plus / Plus

Query: 201 caagcttatttcaatgagactgcagacctgccatgccaatgtgcaaactctcaaaaccaa 260

||||| ||||| || || ||||| ||||| ||||| ||||| |||||  
Sbjct: 117 caagcttatttcaatgggactgcatactctgccgtgccatttacaaggctcaaaacata 176

Query: 261 agcctgagtgcagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320

||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 177 agcctgagtgcagctggttagtattttggcaggaccagcaaaagttggttctgtacgagcac 236

Query: 321 tacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcccgcacaagtttt 380

|| || ||||| ||||| || || ||||| ||||| ||||| ||||| |||||  
Sbjct: 237 tatttgggcacagagaaacttgatagtgtgaatgccaaagtacctgggcccgcacagagcttt 296

Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgat 440

|| || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 297 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgtat 356

Score = 58.0 bits (29), Expect = 1e-04

Identities = 53/61 (86%)

Strand = Plus / Plus

Query: 645 aattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtcacagaactg 704

||||| ||||| || || ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 555 aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 614

Score = 46.1 bits (23), Expect = 0.41  
Identities = 35/39 (89%)  
Strand = Plus / Plus

☐ >gi|4587841|gb|AF065898.1|AF065898 **LU** Mus musculus strain C57BL/6J CD86 antigen  
 Length = 984

Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggttgat 440  
|| ||| |||| | ||||||| ||||||| ||||||| ||||||| ||||||| ||||  
Sbjct: 297 gagaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggcctgat 356

```

Query:  705  t  705
        |
Sbjct:  615  t  615

```

Score = 46.1 bits (23), Expect = 0.41  
Identities = 35/39 (89%)  
Strand = Plus / Plus

Query: 501 gaactgtcagtgcttgctaacttcagtcaacctgaaata 539  
          |||||  
Sbjct: 417 gaactgtcagtgatcgccaacttcagtgaacctgaaata 455

☐ >gi|4587839|gb|AF065897.1|AF065897 **LU** Mus musculus strain A/J CD86 antigen (Cd8  
          Length = 984

Score = 143 bits (72), Expect = 2e-30  
Identities = 198/240 (82%)  
Strand = Plus / Plus

Query: 201 caagcttatttcaatgagactgcagacctgccatgccaatgtgcaaactctcaaaaccaa 260  
          |||||  
Sbjct: 117 caagcttatttcaatgggactgcatactgcctgtgccatttacaaggctcaaaacata 176

Query: 261 agcctgagttagcttagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320  
          |||||  
Sbjct: 177 agcctgagttagctggtagtattttggcaggaccagcaaaagttggttctgtacgagcac 236

Query: 321 tacttaggcaaagagaaatttgacagtggtcattccaagtatatgggccgcacaagtttt 380  
          || || |||| ||||| |||| |||| || ||||| ||||| || ||||  
Sbjct: 237 tatttgggcacagagaaacttgatagtgtgaatgccaaagtacctgggccgcacgagcttt 296

Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgtat 440  
          || || |||| ||||| || ||||| ||||| ||||| ||||| |||||  
Sbjct: 297 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgtat 356

Score = 58.0 bits (29), Expect = 1e-04  
Identities = 53/61 (86%)  
Strand = Plus / Plus

Query: 645 aattcaactatcgagtatgatgggtattatgcagaaatctcaagataatgtcacagaactg 704  
          |||||  
Sbjct: 555 aattcaactaatgagtatgggtgataacatgcagatatcacaagataatgtcacagaactg 614

Query: 705 t 705  
          |  
Sbjct: 615 t 615

Score = 46.1 bits (23), Expect = 0.41  
Identities = 35/39 (89%)

Strand = Plus / Plus

Query: 501 gaactgtcagtgccttgctaacttcagtcaacctgaaata 539  
 |||||  
 Sbjct: 417 gaactgtcagtgatcgccaacttcagtgaacctgaaata 455

☐ >gi|1127750|gb|U39462.1|MMB72G07 ☒ Mus musculus B7-2 gene, exon 7  
 Length = 420

Score = 143 bits (72), Expect = 2e-30  
 Identities = 198/240 (82%)  
 Strand = Plus / Plus

Query: 201 caagcttattttcaatgagactgcagacctgccatgccaatgtgcaaactctcaaaaccaa 260  
 |||||  
 Sbjct: 84 caagcttattttcaatgggactgcatactgcccgtgccatttacaaaggctcaaaacata 143

Query: 261 agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320  
 |||||  
 Sbjct: 144 agcctgagtgagctggttagtattttggcaggaccagcaaaagttggttctgtacgagcac 203

Query: 321 tacttaggcaaagagaaaatttgacagtgttcattccaagtatatgggccgcacaagtttt 380  
 || || |||||  
 Sbjct: 204 tatttgggcacagagaaaacttgatagtgtgaatgccaaagtacctgggccgcacagagcttt 263

Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgtat 440  
 || || |||||  
 Sbjct: 264 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgtat 323

☐ >gi|26348035|dbj|AK079513.1| ☒ ☒ Mus musculus 16 days neonate thymus cDNA, RIKEN  
 enriched library, clone:A130091H03 product:CD86 antigen,  
 full insert sequence  
 Length = 2541

Score = 143 bits (72), Expect = 2e-30  
 Identities = 198/240 (82%)  
 Strand = Plus / Plus

Query: 201 caagcttattttcaatgagactgcagacctgccatgccaatgtgcaaactctcaaaaccaa 260  
 |||||  
 Sbjct: 202 caagcttattttcaatgggactgcatactgcccgtgccatttacaaaggctcaaaacata 261

Query: 261 agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320  
 |||||  
 Sbjct: 262 agcctgagtgagctggttagtattttggcaggaccagcaaaagttggttctgtacgagcac 321

Query: 321 tacttaggcaaagagaaaatttgacagtgttcattccaagtatatgggccgcacaagtttt 380

```

      || || |||| ||||| |||| |||| | ||||| ||||| ||||| |||||
Sbjct: 322 tatttgggcacagagaaacttgatagtgatgaatgccaaagtacctgggccgcacgagcttt 381

Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgat 440
      || | ||| |||| | | ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 382 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgtat 441
```

Score = 58.0 bits (29), Expect = 1e-04  
Identities = 53/61 (86%)  
Strand = Plus / Plus

```

Query: 645 aattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtcacagaactg 704
      ||||| ||||| ||||| || || ||||| || || ||||| ||||| ||||| |||||
Sbjct: 640 aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 699
```

```

Query: 705 t 705
      |
Sbjct: 700 t 700
```

Score = 46.1 bits (23), Expect = 0.41  
Identities = 35/39 (89%)  
Strand = Plus / Plus

```

Query: 501 gaactgtcagtgcttgctaacttcagtcaacctgaaata 539
      ||||| ||||| || || ||||| ||||| ||||| |||||
Sbjct: 502 gaactgtcagtgatcgccaacttcagtgaacctgaaata 540
```

☐ >[gi|432478|gb|L25606.1|MUSB72X](#) **LUG** Murine B7-2 mRNA, complete cds  
Length = 1183

Score = 143 bits (72), Expect = 2e-30  
Identities = 198/240 (82%)  
Strand = Plus / Plus

```

Query: 201 caagcttatttcaatgagactgcagacctgccatgccaaatttgcaaactctcaaaaccaa 260
      ||||| ||||| ||||| || || ||||| || || ||||| ||||| ||||| |||||
Sbjct: 183 caagcttatttcaatgggactgcatacttgccgtgccatttacaaaggctcaaaacata 242
```

```

Query: 261 agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 243 agcctgagtgagctggttagtattttggcaggaccagcaaaagttggttctgtacgagcac 302
```

```

Query: 321 tacttaggcaaagagaaatttgacagtggttcattccaagtatatgggccgcacaagtttt 380
      || || |||| ||||| ||||| || || ||||| ||||| ||||| ||||| |||||
Sbjct: 303 tatttgggcacagagaaacttgatagtgatgaatgccaaagtacctgggccgcacgagcttt 362
```

Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgat 440  
|| | ||| |||| | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 363 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgtat 422

Score = 58.0 bits (29), Expect = 1e-04  
Identities = 53/61 (86%)  
Strand = Plus / Plus

Query: 645 aattcaactatcgagtatgatggattatgcagaaatctcaagataatgtcacagaactg 704  
||||| ||||| ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 621 aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 680

Query: 705 t 705  
|  
Sbjct: 681 t 681

Score = 46.1 bits (23), Expect = 0.41  
Identities = 35/39 (89%)  
Strand = Plus / Plus

Query: 501 gaactgtcagtgcttgctaacttcagtcaacctgaaata 539  
||||| ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 483 gaactgtcagtgatcgccaacttcagtgaacctgaaata 521

☐ >gi|546694|gb|S70108.1|S70108 **L** early T cell costimulatory molecule-1 [mice, 5C2  
mRNA, 1115 nt]  
Length = 1115

Score = 143 bits (72), Expect = 2e-30  
Identities = 198/240 (82%)  
Strand = Plus / Plus

Query: 201 caagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaaaaccaa 260  
||||| ||||| ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 166 caagcttatttcaatgggactgcatactgcccgtgccatttataaaggctcaaaacata 225

Query: 261 agcctgagtgagctagtagtattttggcaggaccagaaaacttggttctgaatgaggta 320  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 226 agcctgagtgagctggttagtattttggcaggaccagaaaagtgggttctgtacgagcac 285

Query: 321 tacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcacaagtttt 380  
|| || |||| ||||| ||||| ||||| || || ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 286 tatttgggcacagagaaacttgatagtgtgaatgccaagtacctgggccgcacgagcttt 345

Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgat 440  
|| | ||| |||| | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 346 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgtat 405

7/9/2004



Score = 58.0 bits (29), Expect = 1e-04  
Identities = 53/61 (86%)  
Strand = Plus / Plus

Query: 645 aattcaactatcgagtatgatgggtattatgcagaaatctcaagataatgtcacagaactg 704  
||||||| ||||| || || ||||| ||| ||||| ||||| |||||  
Sbjct: 613 aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 672

Query: 705 t 705  
|  
Sbjct: 673 t 673

☐ >gi|31542363|ref|NM\_019388.2| **LUG** Mus musculus CD86 antigen (Cd86), mRNA  
Length = 2528

Score = 141 bits (71), Expect = 9e-30  
Identities = 194/235 (82%)  
Strand = Plus / Plus

Query: 201 caagcttatttcaatgagactgcagacctgccatgccaatgtgcaaactctcaaaaccaa 260  
||||||| ||||| | |||| | |||| | |||| | |||| | ||||  
Sbjct: 175 caagcttatttcaatgggactgcatactgccgtgccatttacaagggtcaaaacata 234

Query: 261 agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320  
||||||| ||||| ||||| ||||| |||| | |||| | |||| | ||||  
Sbjct: 235 agcctgagtgagctggttagtattttggcaggaccagcaaaagtgggttctgtacgagcac 294

Query: 321 tacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcacaagtttt 380  
|| || |||| ||||| |||| |||| | |||| | |||| | ||||  
Sbjct: 295 tatttgggcacagagaaacttgatagtgtgaatgccaaagtacctgggccgcacagagcttt 354

Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggct 435  
|| | ||| |||| | ||||| ||||| ||||| ||||| |||||  
Sbjct: 355 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggct 409

Score = 58.0 bits (29), Expect = 1e-04  
Identities = 53/61 (86%)  
Strand = Plus / Plus

Query: 645 aattcaactatcgagtatgatgggtattatgcagaaatctcaagataatgtcacagaactg 704  
||||||| ||||| || || ||||| ||| ||||| ||||| |||||  
Sbjct: 613 aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 672

Query: 705 t 705  
|  
Sbjct: 673 t 673

☐ >[gi|808027|gb|U17717.1|HSB72S3](#) Human CTLA-4 counter-receptor B7.2 (B7.2) gene, ε  
Length = 484

Score = 105 bits (53), Expect = 5e-19  
Identities = 53/53 (100%)  
Strand = Plus / Plus

Query: 130 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggt 182  
|||||  
Sbjct: 260 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggt 312

☐ >[gi|25188157|dbj|AB085744.1|](#) Mesocricetus auratus mRNA for B7-2, complete cds  
Length = 2611

Score = 101 bits (51), Expect = 8e-18  
Identities = 84/95 (88%)  
Strand = Plus / Plus

Query: 201 caagcttatttcaatgagactgcagacctgccatgccaatgtgcaaactctcaaaaccaa 260  
|||||  
Sbjct: 183 caagcttatttcaataggactgcatacctgccatgccattacaaaggctcaaaataga 242

Query: 261 agcctgagttagcttagtagtattttggcaggacca 295  
|||||  
Sbjct: 243 agcctgagttagctgtagtagtattttggcaggacca 277

Score = 56.0 bits (28), Expect = 4e-04  
Identities = 58/68 (85%)  
Strand = Plus / Plus

Query: 672 atgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctgtt 731  
|||||  
Sbjct: 654 atgcagatatcacaagacaatgtcacagaactgttcagcgtttccattagcctgtctatt 713

Query: 732 tcattccc 739  
|||||  
Sbjct: 714 ccattccc 721

Score = 48.1 bits (24), Expect = 0.10  
Identities = 39/44 (88%)  
Strand = Plus / Plus

Query: 572 cataaatttgacctgctcatctatacacggttaccagaaccta 615  
|||||  
Sbjct: 551 cataaatttgacctgctcatctaaagaaggttatccaaaaccta 594

Score = 48.1 bits (24), Expect = 0.10  
 Identities = 30/32 (93%)  
 Strand = Plus / Plus

Query: 403 gacttcacaatcttcagatcaaggacaagggc 434  
 |||||  
 Sbjct: 385 gacttcacaatgttcagatcaaggacatgggc 416

Score = 44.1 bits (22), Expect = 1.6  
 Identities = 31/34 (91%)  
 Strand = Plus / Plus

Query: 507 tcagtgccttgctaacttcagtcaacctgaaatag 540  
 |||||  
 Sbjct: 489 tcagtgatggctaacttcagtgaacctgaaatag 522

☐ >[gi|808031|gb|U17721.1|HSB72S7](#) Human CTLA-4 counter-receptor B7.2 (B7.2) gene, c  
 Length = 658

Score = 93.7 bits (47), Expect = 2e-15  
 Identities = 47/47 (100%)  
 Strand = Plus / Plus

Query: 963 ggaaccaacacaatggagaggggaagagagtgaacagaccaagaaaag 1009  
 |||||  
 Sbjct: 273 ggaaccaacacaatggagaggggaagagagtgaacagaccaagaaaag 319

☐ >[gi|3851167|gb|AF099105.1|AF099105](#) Homo sapiens B7.2 antigen (CD86) gene, promot  
 Length = 1277

Score = 85.7 bits (43), Expect = 5e-13  
 Identities = 43/43 (100%)  
 Strand = Plus / Plus

Query: 1 ggaaggcttgacaggggtgaaagctttgcttctctgctgctgt 43  
 |||||  
 Sbjct: 1235 ggaaggcttgacaggggtgaaagctttgcttctctgctgctgt 1277

☐ >[gi|44889504|gb|AY533858.1|](#) **LU** Bos taurus CD86 mRNA, 3' UTR and partial cds  
 Length = 2062

Score = 79.8 bits (40), Expect = 3e-11  
 Identities = 68/76 (89%), Gaps = 1/76 (1%)  
 Strand = Plus / Plus

```
Query: 1572 atgaccttatagtgtt 1587
      ||| ||||| |||
Sbjct: 746 atggccttataatgtt 761
```

Score = 69.9 bits (35), Expect = 3e-08  
Identities = 142/174 (81%), Gaps = 4/174 (2%)  
Strand = Plus / Plus

Query: 2114 cagggagggggttttggtgatacccaagtatttgggatgt--catcttcctggaagcagag 2171  
 |||  
 Spict: 1291 t-gggaggggttttgatgatagccagcttgttgtaattgttcacccgactggaagcagag 1349

Query: 2172 ctggggaggaggagagccatcaccttgataatgggatgaatggaaggaggccttagg 2225  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 1350 ctgggaaggaggagagctatcatcttaataacgggggtg-atggaaggaggccttagg 1402

Score = 52.0 bits (26), Expect = 0.007  
Identities = 65/78 (83%)  
Strand = Plus / Plus

Query: 1662 taaggagttctcatccctctgtcagggtcagtaaggaaaacggtggcctagggtaggc 1721  
|||||  
Sbict: 823 taaggaattctggtccctctgtgagggtcagtaaggaaagtgatggtccagtatgctgac 882

```
Query: 1722 aacaatgagcagaccaac 1739
          |||||
Sbjct: 883 aacaatgagcagaccaac 900
```

Score = 52.0 bits (26), Expect = 0.007  
Identities = 107/134 (79%)  
Strand = Plus / Plus

Query: 985    aagagagtgtaacagaccaagaaaagagaaaaaatccatatacctgaaagatctgatgaag    1044  
 |||  
 Sbjct: 162    aagagagtgtaacagactgcgaaaagagtgaactccaagaacctgaaagatctgatgaag    221

Query: 1045 cccagcgtgttttttaaagttcgaagacatcttcatgcgacaaaagtgatacatgttttt 1104

Sbjct: 222      ||||| ||| | ||||| | ||| ||||| | |||      ||||| | ||||| ||| |  
tccagtgtgatgttaacatttcaaagacagcctcagataacaaaagcgctacaaatttgt 281

Query: 1105 aattaaagagtaaa 1118

||||| ||||| |||||  
Sbjct: 282 aattaaagagtaaa 295

☐ >gi|11464988|ref|NM\_020081.1| **LUG** Rattus norvegicus CD86 antigen (Cd86), mRNA  
Length = 942

Score = 73.8 bits (37), Expect = 2e-09  
Identities = 115/141 (81%)  
Strand = Plus / Plus

Query: 171 ctgctctctggtgctgctcctctgaagattcaagcttatttcaatgagactgcagacctg 230  
||||| ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 70 ctgctctcagatgctgttctctgtgaagaggcaagcttacttcaatagcactgcatacctg 129

Query: 231 ccatgccaatgtgcaaactctcaaaaccaaagcctgagtgagctagtagtattttggcag 290  
|| |||| | | |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 130 ccgtgcccgttcacaaaggctcaaaacataagcccgagtgagctcgtagtagtattttggcag 189

Query: 291 gaccaggaaaacttggttctg 311  
|||| | |||| | |||||  
Sbjct: 190 gaccggaaaaagtcggttctg 210

Score = 60.0 bits (30), Expect = 3e-05  
Identities = 36/38 (94%)  
Strand = Plus / Plus

Query: 403 gacttcacaatcttcagatcaaggacaagggcttgtat 440  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 302 gacttcacaatgttcagatcaaggacacgggcttgtat 339

Score = 46.1 bits (23), Expect = 0.41  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 572 cataaatttgacctgctcatcta 594  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 471 cataaatttgacctgctcatcta 493

☐ >gi|2627024|dbj|D50558.1| **LUG** Rattus norvegicus mRNA for membrane glycoprotein  
Length = 942

Score = 73.8 bits (37), Expect = 2e-09  
Identities = 115/141 (81%)  
Strand = Plus / Plus

Query: 171 ctgctctctgggtgctgctcctctgaagattcaagcttatttcaatgagactgcagacctg 230  
||||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 70 ctgctctcagatgctgttcctgtgaagaggcaagcttacttcaatagcactgcataacctg 129

Query: 231 ccattgccaatttgcaaactctcaaaaccaaagcctgagttagcttagtagtattttggcag 290  
|| |||| | | |||| | ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 130 ccgtgcccgttcacaaaggctcaaaacataagcccgagttagcttagtagtattttggcag 189

Query: 291 gaccaggaaaacttggttctg 311  
|||| | |||| | |||||  
Sbjct: 190 gaccggaaaaagtcggttctg 210

Score = 60.0 bits (30), Expect = 3e-05  
Identities = 36/38 (94%)  
Strand = Plus / Plus

Query: 403 gacttcacaatcttcagatcaaggacaagggttgtat 440  
||||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 302 gacttcacaatgttcagatcaaggacacgggttgtat 339

Score = 46.1 bits (23), Expect = 0.41  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 572 cataaatttgacctgctcatcta 594  
||||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 471 cataaatttgacctgctcatcta 493

☐ >gi|940936|gb|U31330.1|RNU31330 **LU** Rattus norvegicus B7-2 mRNA, partial cds  
Length = 449

Score = 63.9 bits (32), Expect = 2e-06  
Identities = 47/52 (90%)  
Strand = Plus / Plus

Query: 260 aagcctgagttagcttagtagtattttggcaggaccaggaaaacttggttctg 311  
||||||| ||||| ||||| ||||| ||||| ||||| |||||  
Sbjct: 5 aagcctgagttagcttagtagtattttggcaggaccaggaaaagtcggttctg 56

Score = 60.0 bits (30), Expect = 3e-05  
Identities = 36/38 (94%)  
Strand = Plus / Plus

Query: 403 gacttcacaatcttcagatcaaggacaagggcttgat 440  
|||||||  
Sbjct: 148 gacttcacaatgttcagatcaaggacacgggcttgat 185

Score = 46.1 bits (23), Expect = 0.41  
Identities = 23/23 (100%)  
Strand = Plus / Plus

Query: 572 cataaatttgacctgctcatcta 594  
|||||||  
Sbjct: 317 cataaatttgacctgctcatcta 339

Score = 44.1 bits (22), Expect = 1.6  
Identities = 31/34 (91%)  
Strand = Plus / Plus

Query: 672 atgcagaaatctcaagataatgtcacagaactgt 705  
|||||||  
Sbjct: 411 atgcagatatcacaagacaatgtcacagaactgt 444

☐ >gi|1127751|gb|U39463.1|MMB72G08 ☒ Mus musculus B7-2 gene, exon 8  
Length = 418

Score = 58.0 bits (29), Expect = 1e-04  
Identities = 53/61 (86%)  
Strand = Plus / Plus

Query: 645 aattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtcacagaactg 704  
|||||||  
Sbjct: 172 aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 231

Query: 705 t 705  
|  
Sbjct: 232 t 232

☐ >gi|21217730|gb|AY095931.1| Meriones unguiculatus costimulatory molecule B7.2 mRNA  
cds  
Length = 1040

Score = 50.1 bits (25), Expect = 0.026  
Identities = 49/57 (85%)  
Strand = Plus / Plus

Query: 261 agcctgagttagcttagtagtattttggcaggaccaggaaaacttggttctgaatgag 317

7/9/2004



Gap Penalties: Existence: 5, Extension: 2  
Number of Sequences: 2280493  
Number of Hits to DB: 34,755,694  
Number of extensions: 2119444  
Number of successful extensions: 12565  
Number of sequences better than 10.0: 23  
Number of HSP's better than 10.0 without gapping: 23  
Number of HSP's gapped: 12561  
Number of HSP's successfully gapped: 44  
Number of extra gapped extensions for HSPs above 10.0: 12497  
Length of query: 2781  
Length of database: 11,051,402,435  
Length adjustment: 23  
Effective length of query: 2758  
Effective length of database: 10,998,951,096  
Effective search space: 30335107122768  
Effective search space used: 30335107122768  
A: 0  
X1: 11 (21.8 bits)  
X2: 15 (30.0 bits)  
X3: 25 (50.0 bits)  
S1: 12 (25.0 bits)  
S2: 21 (42.1 bits)

C

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Bennett et al.

Serial No.: 10/444,206

Filed: May 23, 2003

For: Oligonucleotide Compositions  
and Methods for the Modulation of  
the Expression of B7 Protein

Group Art Unit: 1635

Examiner: To be Assigned

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) Laura Frasher  
) Laura Frasher

**REQUEST FOR CONVERSION OF NONPROVISIONAL APPLICATION TO A  
PROVISIONAL APPLICATION PURSUANT TO 37 C.F.R. 1.53(C)(2)**

Mail Stop Conversion  
Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Sir:

The Applicants hereby request that U.S. Application Serial No. 10/444,206  
be converted to a U.S. Provisional Patent Application pursuant to 37 C.F.R. 1.53(c)(2).

The Applicants submit herewith the fee for this request under 1.17(q). The  
Commissioner is hereby authorized to charge any additional fees which may be required  
to Deposit Account No. 13-2855. A duplicate of this paper is enclosed.

Respectfully submitted,

MARSHALL, GERSTEIN &amp; BORUN LLP

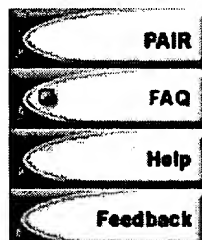
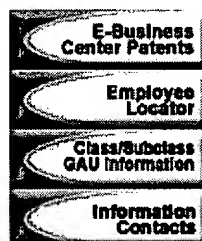
By

March 9, 2004

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Application Number:	10/444,206	Customer Number:	-
Filing or 371(c) Date:	05-23-2003	Status:	Docketed New Case - for Examination
Application Type:	Utility	Status Date:	04-20-2004
Examiner Name:	EPPS FORD, JANET L	Location:	ELECTRONIC
Group Art Unit:	1635	Location Date:	-
Confirmation Number:	5228	Earliest Publication No:	US 2004-0023917 A1
Attorney Docket Number:	30566/39365	Earliest Publication Date:	02-05-2004
Class/ Sub-Class:	514/044	Patent Number:	-
First Named Inventor:	C. Bennett, Carlsbad, CA (US)	Issue Date of Patent:	-
Title Of Invention:	Oligonucleotide compositions and methods for the modulation expression of B7 protein		

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Assignments

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Published Documents

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File History	
Date	Contents Description
04-29-2004	Correspondence Address Change
09-29-2003	New or Additional Drawing Filed
04-20-2004	IFW TSS Processing by Tech Center Complete
08-18-2003	Preliminary Amendment
04-20-2004	Case Docketed to Examiner in GAU
10-08-2003	Application Dispatched from OIPE
10-09-2003	Application Is Now Complete
09-24-2003	Additional Application Filing Fees
09-24-2003	A statement by one or more inventors satisfying the requirement under 37 CFR 1.15, Oath of the Applicant
09-24-2003	Applicant has submitted new drawings to correct Corrected Papers
07-24-2003	Notice Mailed--Application Incomplete--Filing Date Assigned
06-13-2003	CRF Is Good Technically / Entered into Database
06-11-2003	Cleared by OIPE CSR
06-11-2003	Cleared by OIPE CSR

06-06-2003	IFW Scan & PACR Auto Security Review
06-04-2003	IFW Scan & PACR Auto Security Review
05-23-2003	CRF Disk Has Been Received by Preexam / Group / PCT
05-23-2003	Initial Exam Team nn

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